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OM protein - protein search, using sw model

Run on: December 5, 2003, 14:26:38 ; Search time 35.3599 Seconds
(without alignments)
3196.087 Million cell updates/sec

Title: US-09-854-356-7
Perfect score: 3954
Sequence: 1 MELAALCRWGLLLALLPPGA.....GFFCPDPAPGAGGMVHHRHR 712

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_19Jun03:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3954	100.0	712	21	AAB21204	Human HER-2/neu fu
2	3954	100.0	712	23	AAM51149	Her-2/neu extracel
3	3954	100.0	919	21	AAB21203	Human HER-2/neu fu
4	3954	100.0	919	23	AAM51148	Her-2/neu extracel
5	3776	95.5	1200	21	AAB21208	Human HER-2/neu pr
6	3776	95.5	1255	17	AAW01111	HER-2/neu protein.
7	3776	95.5	1255	20	AAW92406	Human HER-2/neu on
8	3776	95.5	1255	21	AAB21198	Human HER-2/neu pr
9	3776	95.5	1255	21	AAY84780	Amino acid sequenc
10	3776	95.5	1255	21	AAY92620	Human heregulin 2
11	3776	95.5	1255	22	AAE12130	Human tyrosine kin
12	3776	95.5	1255	22	AAB85458	Human HER-2/neu pr
13	3776	95.5	1255	22	AAG88267	HER2/neu amino aci
14	3776	95.5	1255	22	AAB60167	HER2 transgene pla
15	3776	95.5	1255	23	AAE26349	Human HER-2 protei
16	3776	95.5	1255	23	AAE26366	Human Her2 antigen
17	3776	95.5	1255	23	AAE24067	Human Her-2 protei
18	3776	95.5	1255	23	AAE20479	Human Her-2/neu pr
19	3776	95.5	1255	23	AAM51143	Human Her-2/neu on
20	3776	95.5	1255	23	AAU77114	Human Her-2/neu po
21	3776	95.5	1255	23	AAU74545	Human HER2 (ErbB2)
22	3776	95.5	1255	24	ABR47447	Breast cancer asso
23	3776	95.5	1255	24	ABP74708	Human Her2/Neu pro
24	3733	94.4	1433	14	AAR39568	Sequence of c-erbB
25	3632	91.9	782	18	AAW19764	Her2-GM-CSF immuno
26	3628	91.8	653	21	AAB21200	Extracellular HER-
27	3628	91.8	653	23	AAM51145	Human Her-2/neu on
28	3606	91.2	1223	23	AAU98923	Human breast cance
29	3590	90.8	645	22	AAB60408	Human ErbB2 oncopr
30	3590	90.8	645	22	AAB61593	Human ErbB2 extrac
31	3590	90.8	645	23	ABG70753	Human HER2 recepto
32	3525	89.2	951	21	AAY44993	DC8scFv-erbB2EC fu
33	3422	86.5	624	11	AAR08222	Extracellular port
34	3373.5	85.3	920	23	AAM51152	Mouse Her-2/neu ex
35	3373.5	85.3	926	23	AAM51153	Mouse Her-2/neu ex
36	3209.5	81.2	1256	21	AAB21199	Rat HER-2/neu prot
37	3209.5	81.2	1256	23	AAM51144	Rat Her-2/neu onco
38	3189.5	80.7	1256	21	AAB21206	Mouse Her-2/neu pr
39	3189.5	80.7	1256	22	AAG62860	Amino acid sequenc
40	3189.5	80.7	1256	23	AAM51151	Mouse Her-2/neu on
41	3110.5	78.7	654	21	AAB21205	Rat HER-2/neu prot
42	3110.5	78.7	654	23	AAM51150	Rat Her-2/neu onco
43	1827	46.2	420	21	AAY97240	Truncated HER-2, p
44	1825.5	46.2	419	22	AAE09207	Human p68HER-2 gen
45	1824.5	46.1	419	23	AAE20348	Human truncated HE

ALIGNMENTS

RESULT 1
AAB21204
ID AAB21204 standard; protein; 712 AA.
XX
AC AAB21204;
XX
DT 12-JAN-2001 (first entry)
XX
DE Human HER-2/neu fusion protein.
XX
KW Human; HER-2/neu; oncogene; tyrosine kinase; cytostatic; vaccine;
KW breast cancer; prostate cancer; ovarian cancer; lung cancer;
KW colon cancer; fusion protein.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200044899-A1.
XX
PD 03-AUG-2000.
XX
PF 28-JAN-2000; 2000WO-US02164.
XX
PR 29-JAN-1999; 99US-0117976.
XX
PA (CORI-) CORIXA CORP.
PA (SMIK) SMITHKLINE BEECHAM.
XX
PI Cheever MA, Gheysen D;
XX
DR WPI; 2000-505976/45.
XX

```
PT   HER-2/neu extracellular domain/phosphorylation domain fusion proteins
PT   useful for vaccinating against breast, ovarian, colon, lung and
PT   prostate cancers -
XX
PS   Claim 27; Fig 13; 128pp; English.
XX
CC   The present sequence is a fusion protein comprising the extracellular
CC   domain and a preferred portion of the phosphorylation domain of the human
CC   HER-2/neu protein. HER-2/neu is a member of the tyrosine kinase family of
CC   receptor-like glycoproteins and shows homology to the epidermal growth
CC   factor receptor (EGFR). It probably plays a part in cell growth and/or
CC   differentiation. The HER-2/neu gene is an oncogene. HER-2/neu fusion
CC   proteins may be used to treat or prevent cancer by eliciting or enhancing
CC   an immune response to the HER-2/neu protein. They may be used to treat
CC   malignancies such as breast, ovarian, colon, lung and prostate cancers,
CC   and may be used as an antigen to vaccinate against these neoplasias.
XX
SQ   Sequence   712 AA;

  Query Match            100.0%;  Score 3954;  DB 21;  Length 712;
  Best Local Similarity  100.0%;  Pred. No. 4.2e-299;
  Matches  712;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60
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Db        121 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180

Qy        181 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240
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Db        181 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240

Qy        241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300

Qy        301 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360
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Db        301 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360

Qy        361 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP 420

Qy        421 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 480
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Db        421 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 480

Qy        481 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC 540
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Qy        541 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC 600
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Qy        661 ASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHR 712
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Db        661 ASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHR 712


RESULT 2
AAM51149
ID   AAM51149 standard; Protein; 712 AA.
XX
AC   AAM51149;
XX
DT   17-JUN-2002  (first entry)
XX
DE   Her-2/neu extracellular domain-delta-phosphorylation domain fusion.
XX
KW   Her-2/neu; oncogene; cancer; tumour; vaccine; human; p185;
KW   tyrosine kinase; receptor; c-erbB2; gene therapy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Domain          1..653
FT                   /note= "extracellular domain"
FT   Domain          654..712
FT                   /note= "phosphorylation domain fragment"
XX
PN   WO200212341-A2.
XX
PD   14-FEB-2002.
XX
PF   03-AUG-2001; 2001WO-US24283.
XX
PR   03-AUG-2000; 2000US-0632507.
XX
PA   (CORI-) CORIXA CORP.
PA   (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI   Cheever MA,  Gheysen D;
XX
DR   WPI; 2002-241743/29.
XX
PT   Her-2/neu fusion protein for treating or preventing cancer by eliciting
PT   or enhancing an immune response to the protein, has Her-2/neu
PT   extracellular domain fused to Her-2/neu intracellular or
PT   phosphorylation domain  -
XX
PS   Claim 37; Fig 13; 141pp; English.
XX
CC   The present sequence is that of a fusion protein between the
CC   extracellular domain and a fragment (DeltaPD) of the phosphorylation
CC   domain of human Her-2/neu (see AAM51143), an oncogenic self-protein
CC   and target for anti-cancer vaccines.  The fusion protein can be
CC   obtained by recombinant DNA methods.  Her-2/neu overexpression
CC   correlates with a poor prognosis in breast and ovarian cancers.
CC   The invention provides Her-2/neu fusion proteins, nucleic acids
CC   encoding them, viral vectors, and vaccines comprising the fusion
CC   proteins or nucleic acid molecules.  In preferred fusion proteins,
CC   the extracellular domain of Her-2/neu is fused to a Her-2/neu
CC   intracellular domain or phosphorylation domain (or its DeltaPD
CC   fragment).  An immune response to Her-2/neu protein is elicited or
CC   enhanced by administering the fusion protein in the form of a vaccine,
CC   or by transfecting cells of an animal ex vivo with a nucleic acid
CC   encoding the fusion protein, and delivering the transfected cells
CC   to the animal.  The fusion proteins, nucleic acids, and isolated
CC   specific T-cells are useful for inhibiting the development of a
CC   cancer, especially breast, ovarian, colon, lung or prostate cancer
CC   in a patient.  T cells that specifically react with a Her-2/neu
CC   fusion protein can be used to remove tumour cells from a sample in
CC   order to inhibit the development of cancer in a patient.
XX
SQ   Sequence   712 AA;

  Query Match            100.0%;  Score 3954;  DB 23;  Length 712;
  Best Local Similarity  100.0%;  Pred. No. 4.2e-299;
  Matches  712;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         121 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180
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Qy         181 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240
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Qy         361 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP 420

Qy         421 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 480

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Qy         661 ASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHR 712
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Db         661 ASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHR 712


RESULT 3
AAB21203
ID   AAB21203 standard; protein; 919 AA.
XX
AC   AAB21203;
XX
DT   12-JAN-2001  (first entry)
XX
DE   Human HER-2/neu fusion protein.
XX
KW   Human; HER-2/neu; oncogene; tyrosine kinase; cytostatic; vaccine;
KW   breast cancer; prostate cancer; ovarian cancer; lung cancer;
KW   colon cancer; fusion protein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200044899-A1.
XX
PD   03-AUG-2000.
XX
PF   28-JAN-2000; 2000WO-US02164.
XX
PR   29-JAN-1999;   99US-0117976.
XX
PA   (CORI-) CORIXA CORP.
PA   (SMIK ) SMITHKLINE BEECHAM.
XX
PI   Cheever MA,  Gheysen D;
XX
DR   WPI; 2000-505976/45.
XX
PT   HER-2/neu extracellular domain/phosphorylation domain fusion proteins
PT   useful for vaccinating against breast, ovarian, colon, lung and
PT   prostate cancers -
XX
PS   Claim 2; Fig 12; 128pp; English.
XX
CC   The present sequence is a fusion protein comprising the extracellular
CC   domain and the phosphorylation domain of the human HER-2/neu protein.
CC   HER-2/neu is a member of the tyrosine kinase family of receptor-like
CC   glycoproteins and shows homology to the epidermal growth factor receptor
CC   (EGFR). It probably plays a part in cell growth and/or differentiation.
CC   The HER-2/neu gene is an oncogene. HER-2/neu fusion proteins may be used
CC   to treat or prevent cancer by eliciting or enhancing an immune response
CC   to the HER-2/neu protein. They may be used to treat malignancies such as
CC   breast, ovarian, colon, lung and prostate cancers, and may be used as an
CC   antigen to vaccinate against these neoplasias.
XX
SQ   Sequence   919 AA;

  Query Match             100.0%;  Score 3954;  DB 21;  Length 919;
  Best Local Similarity   100.0%;  Pred. No. 6e-299;
  Matches  712;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy          61 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120
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Qy         241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300
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Qy         301 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360
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Qy         361 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP 420
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Qy         421 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 480
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Qy         481 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC 540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC 540

Qy         541 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC 600
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC 600

Qy         601 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSQNEDLGP 660
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSQNEDLGP 660

Qy         661 ASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHR 712
```

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                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHR 712


RESULT 4
AAM51148
ID   AAM51148 standard; Protein; 919 AA.
XX
AC   AAM51148;
XX
DT   17-JUN-2002  (first entry)
XX
DE   Her-2/neu extracellular domain-phosphorylation domain fusion.
XX
KW   Her-2/neu; oncogene; cancer; tumour; vaccine; human; p185;
KW   tyrosine kinase; receptor; c-erbB2; gene therapy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Domain          1..653
FT                   /note= "extracellular domain"
FT   Domain          654..919
FT                   /note= "phosphorylation domain"
XX
PN   WO200212341-A2.
XX
PD   14-FEB-2002.
XX
PF   03-AUG-2001; 2001WO-US24283.
XX
PR   03-AUG-2000; 2000US-0632507.
XX
PA   (CORI-) CORIXA CORP.
PA   (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI   Cheever MA,  Gheysen D;
XX
DR   WPI; 2002-241743/29.
XX
PT   Her-2/neu fusion protein for treating or preventing cancer by eliciting
PT   or enhancing an immune response to the protein, has Her-2/neu
PT   extracellular domain fused to Her-2/neu intracellular or
PT   phosphorylation domain  -
XX
PS   Claim 2; Fig 12; 141pp; English.
XX
CC   The present sequence is that of a fusion protein between the
CC   extracellular domain and phosphorylation domain of human Her-2/neu
CC   (see AAM51143), an oncogenic self-protein and target for anti-cancer
CC   vaccines.  The fusion protein can be obtained by recombinant DNA
CC   methods.  Her-2/neu overexpression correlates with a poor prognosis
CC   in breast and ovarian cancers.  The invention provides Her-2/neu
CC   fusion proteins, nucleic acids encoding them, viral vectors, and
CC   vaccines comprising the fusion proteins or nucleic acid molecules.
CC   In preferred fusion proteins, the extracellular domain of a
CC   Her-2/neu protein is fused to a Her-2/neu intracellular domain or
CC   phosphorylation domain (or its DeltaPD fragment).  An immune
CC   response to Her-2/neu protein is elicited or enhanced by
CC   administering the fusion protein in the form of a vaccine, or by
CC   transfecting cells of an animal ex vivo with a nucleic acid
CC   encoding the fusion protein, and delivering the transfected cells
CC   to the animal.  The fusion proteins, nucleic acids, and isolated
CC   specific T-cells are useful for inhibiting the development of a
CC   cancer, especially breast, ovarian, colon, lung or prostate cancer
CC   in a patient.  T cells that specifically react with a Her-2/neu
CC   fusion protein can be used to remove tumour cells from a sample in
CC   order to inhibit the development of cancer in a patient.
XX
SQ   Sequence   919 AA;

  Query Match             100.0%;  Score 3954;  DB 23;  Length 919;
  Best Local Similarity   100.0%;  Pred. No. 6e-299;
```

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  Matches  712;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60

Qy         61 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120

Qy        121 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180

Qy        181 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240

Qy        241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300

Qy        301 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360

Qy        361 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP 420

Qy        421 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 480

Qy        481 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC 540

Qy        541 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC 600

Qy        601 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSQNEDLGP 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSQNEDLGP 660

Qy        661 ASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHR 712
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHR 712


RESULT 5
AAB21208
ID   AAB21208 standard; Protein; 1200 AA.
XX
AC   AAB21208;
XX
DT   12-JAN-2001  (first entry)
XX
DE   Human HER-2/neu protein.
XX
KW   Human; HER-2/neu; oncogene; tyrosine kinase; cytostatic; vaccine;
KW   breast cancer; prostate cancer; ovarian cancer; lung cancer;
KW   colon cancer.
XX
OS   Homo sapiens.
XX
PN   WO200044899-A1.
XX
PD   03-AUG-2000.
XX
PF   28-JAN-2000; 2000WO-US02164.
XX
```

```
PR   29-JAN-1999;   99US-0117976.
XX
PA   (CORI-) CORIXA CORP.
PA   (SMIK ) SMITHKLINE BEECHAM.
XX
PI   Cheever MA,  Gheysen D;
XX
DR   WPI; 2000-505976/45.
DR   N-PSDB; AAA89736.
XX
PT   HER-2/neu extracellular domain/phosphorylation domain fusion proteins
PT   useful for vaccinating against breast, ovarian, colon, lung and
PT   prostate cancers -
XX
PS   Disclosure; Fig 15; 128pp; English.
XX
CC   The present sequence is the human HER-2/neu protein. It is a member
CC   of the tyrosine kinase family of receptor-like glycoproteins and shows
CC   homology to the epidermal growth factor receptor (EGFR). It probably
CC   plays a part in cell growth and/or differentiation. The HER-2/neu
CC   gene is an oncogene. An HER-2/neu fusion protein comprising a
CC   HER-2/neu extracellular domain fused to a HER-2/neu phosphorylation
CC   domain may be used to treat or prevent cancer by eliciting or
CC   enhancing an immune response to the HER-2/neu protein. It may be used
CC   to treat malignancies such as breast, ovarian, colon, lung and
CC   prostate cancers, and may be used as an antigen to vaccinate against
CC   these neoplasias.
XX
SQ   Sequence   1200 AA;

  Query Match             95.5%;  Score 3776;  DB 21;  Length 1200;
  Best Local Similarity   67.9%;  Pred. No. 6.2e-285;
  Matches  712;  Conservative    0;  Mismatches    0;  Indels  336;  Gaps    1;

Qy          1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60

Qy         61 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120

Qy        121 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180

Qy        181 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240

Qy        241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300

Qy        301 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360

Qy        361 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP 420

Qy        421 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 480

Qy        481 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC 540

Qy        541 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC 600

Qy        601 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTS------- 653
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIISAVVG 660

Qy        654 ------------------------------------------------------------ 653

Db        661 ILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETEL 720

Qy        654 ------------------------------------------------------------ 653

Db        721 RKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSP 780

Qy        654 ------------------------------------------------------------ 653

Db        781 YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVR 840

Qy        654 ------------------------------------------------------------ 653

Db        841 LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT 900

Qy        654 ------------------------------------------------------------ 653

Db        901 HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM 960

Qy        654 ----------------------------QNEDLGPASPLDSTFYRSLLEDDDMGDLVDA 684
                                           ||||||||||||||||||||||||||||||
Db        961 IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA 1020

Qy        685 EEYLVPQQGFFCPDPAPGAGGMVHHRHR 712
              ||||||||||||||||||||||||||||
Db       1021 EEYLVPQQGFFCPDPAPGAGGMVHHRHR 1048


RESULT 6
AAW01111
ID   AAW01111 standard; Protein; 1255 AA.
XX
AC   AAW01111;
XX
DT   01-JAN-1997  (first entry)
XX
DE   HER-2/neu protein.
XX
KW   HER-2/neu; c-erbB1; p185; oncogene; tyrosine protein kinase;
KW   breast cancer; ovary cancer; colon cancer; lung cancer;
KW   prostate cancer; immunisation; tumour; vaccine; vector.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Domain          676..1255
FT                   /label= Intracellular_domain
FT                   /note= "claimed domain, useful for immunisation"
XX
PN   WO9630514-A1.
XX
PD   03-OCT-1996.
XX
PF   28-MAR-1996;   96WO-US01689.
XX
PR   31-MAR-1995;   95US-0414417.
XX
PA   (UNIW ) UNIV WASHINGTON.
XX
PI   Cheever MA,  Disis ML;
XX
DR   WPI; 1996-455361/45.
DR   N-PSDB; AAT40739.
XX
PT   DNA encoding HER-2-neu poly:peptide(s) - used for prevention or
PT   treatment of malignancies with which the HER-2/neu oncogene is
PT   associated
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XX
PS   Claim 2; Page 56-61; 71pp; English.
XX
CC   Human HER-2/neu protein (AAW01111), also called p185 or c-erbB2, is
CC   the product of the HER-2/neo oncogene (see also AAT40739). The
CC   protein is over-expressed in various cancers, including breast,
CC   ovarian, colon, lung and prostate. The intracellular domain of the
CC   protein can be used to immunise an animal against a malignancy with
CC   which the oncogene is associated. The polypeptide can be produced
CC   in transformed host cells for use in immunisation. Alternatively,
CC   animal cells are transfected in vivo or ex vivo with a viral vector
CC   that directs expression of the polypeptide.
XX
SQ   Sequence   1255 AA;

  Query Match             95.5%;  Score 3776;  DB 17;  Length 1255;
  Best Local Similarity   67.9%;  Pred. No. 6.6e-285;
  Matches  712;  Conservative    0;  Mismatches    0;  Indels  336;  Gaps    1;

Qy          1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60

Qy         61 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120

Qy        121 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180

Qy        181 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240

Qy        241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300

Qy        301 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360

Qy        361 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP 420

Qy        421 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 480

Qy        481 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC 540

Qy        541 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC 600

Qy        601 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTS------- 653
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIISAVVG 660

Qy        654 ------------------------------------------------------------ 653

Db        661 ILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETEL 720

Qy        654 ------------------------------------------------------------ 653

Db        721 RKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSP 780

Qy        654 ------------------------------------------------------------ 653

Db        781 YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVR 840

Qy        654 ------------------------------------------------------------ 653

Db        841 LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT 900

Qy        654 ------------------------------------------------------------ 653

Db        901 HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM 960

Qy        654 ----------------------------QNEDLGPASPLDSTFYRSLLEDDDMGDLVDA 684
                                           ||||||||||||||||||||||||||||||
Db        961 IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA 1020

Qy        685 EEYLVPQQGFFCPDPAPGAGGMVHHRHR 712
              ||||||||||||||||||||||||||||
Db       1021 EEYLVPQQGFFCPDPAPGAGGMVHHRHR 1048


RESULT 7
AAW92406
ID   AAW92406 standard; Protein; 1255 AA.
XX
AC   AAW92406;
XX
DT   21-APR-1999  (first entry)
XX
DE   Human HER-2/neu oncogene protein.
XX
KW   HER-2/neu; oncogene; immune response; T cell; B cell; immunisation;
KW   malignancy; treatment; tumour.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          676..1255
FT                   /note= "region which elicits immune response"
XX
PN   US5869445-A.
XX
PD   09-FEB-1999.
XX
PF   01-APR-1996;   96US-0625101.
XX
PR   01-APR-1996;   96US-0625101.
PR   17-MAR-1993;   93US-0033644.
PR   12-AUG-1993;   93US-0106112.
PR   31-MAR-1995;   95US-0414417.
XX
PA   (UNIW ) UNIV WASHINGTON.
XX
PI   Cheever MA,  Disis ML;
XX
DR   WPI; 1999-152835/13.
DR   N-PSDB; AAX01912.
XX
PT   Use of HER-2/neu polypeptides - for eliciting an immune response to
PT   an HER-2/neu associated malignancy, particularly for treating or
PT   preventing tumours
XX
PS   Claim 3; Column 31-38; 26pp; English.
XX
CC   This sequence represents the human HER-2/neu oncogene protein. A fragment
CC   of this protein is used in a method for eliciting or enhancing an immune
CC   response to HER-2/neu protein. The polypeptide can stimulate T cells and
CC   B cells to produce an immune response to the HER-2/neu protein. The
CC   method can be used for immunisation against a malignancy in which the
CC   HER-2/neu oncogene is associated and in the treatment of an existing
CC   tumour, or to prevent tumour occurrence or reoccurrence.
XX
SQ   Sequence   1255 AA;

  Query Match             95.5%;  Score 3776;  DB 20;  Length 1255;
```

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  Best Local Similarity   67.9%;  Pred. No. 6.6e-285;
  Matches  712;  Conservative    0;  Mismatches    0;  Indels  336;  Gaps    1;

Qy          1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60

Qy         61 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120

Qy        121 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180

Qy        181 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240

Qy        241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300

Qy        301 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360

Qy        361 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP 420

Qy        421 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 480

Qy        481 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC 540

Qy        541 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC 600

Qy        601 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTS------- 653
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIISAVVG 660

Qy        654 ------------------------------------------------------------ 653

Db        661 ILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETEL 720

Qy        654 ------------------------------------------------------------ 653

Db        721 RKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSP 780

Qy        654 ------------------------------------------------------------ 653

Db        781 YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVR 840

Qy        654 ------------------------------------------------------------ 653

Db        841 LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT 900

Qy        654 ------------------------------------------------------------ 653

Db        901 HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM 960

Qy        654 ----------------------------QNEDLGPASPLDSTFYRSLLEDDDMGDLVDA 684
                                         ||||||||||||||||||||||||||||||
Db        961 IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA 1020

Qy        685 EEYLVPQQGFFCPDPAPGAGGMVHHRHR 712
              ||||||||||||||||||||||||||||
Db       1021 EEYLVPQQGFFCPDPAPGAGGMVHHRHR 1048


RESULT 8
AAB21198
ID   AAB21198 standard; protein; 1255 AA.
XX
AC   AAB21198;
XX
DT   12-JAN-2001  (first entry)
XX
DE   Human HER-2/neu protein.
XX
KW   Human; HER-2/neu; oncogene; tyrosine kinase; cytostatic; vaccine;
KW   breast cancer; prostate cancer; ovarian cancer; lung cancer;
KW   colon cancer.
XX
OS   Homo sapiens.
XX
PN   WO200044899-A1.
XX
PD   03-AUG-2000.
XX
PF   28-JAN-2000; 2000WO-US02164.
XX
PR   29-JAN-1999;   99US-0117976.
XX
PA   (CORI-) CORIXA CORP.
PA   (SMIK ) SMITHKLINE BEECHAM.
XX
PI   Cheever MA,  Gheysen D;
XX
DR   WPI; 2000-505976/45.
DR   N-PSDB; AAA89736.
XX
PT   HER-2/neu extracellular domain/phosphorylation domain fusion proteins
PT   useful for vaccinating against breast, ovarian, colon, lung and
PT   prostate cancers -
XX
PS   Claim 52; Fig 7; 128pp; English.
XX
CC   The present sequence is the human HER-2/neu protein. It is a member of
CC   the tyrosine kinase family of receptor-like glycoproteins and shows
CC   homology to the epidermal growth factor receptor (EGFR). It probably
CC   plays a part in cell growth and/or differentiation. The HER-2/neu
CC   gene is an oncogene. An HER-2/neu fusion protein comprising a
CC   HER-2/neu extracellular domain fused to a HER-2/neu phosphorylation
CC   domain may be used to treat or prevent cancer by eliciting or
CC   enhancing an immune response to the HER-2/neu protein. It may be used
CC   to treat malignancies such as breast, ovarian, colon, lung and
CC   prostate cancers, and may be used as an antigen to vaccinate against
CC   these neoplasias.
XX
SQ   Sequence   1255 AA;

  Query Match             95.5%;  Score 3776;  DB 21;  Length 1255;
  Best Local Similarity   67.9%;  Pred. No. 6.6e-285;
  Matches  712;  Conservative    0;  Mismatches    0;  Indels  336;  Gaps    1;

Qy          1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60

Qy         61 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120

Qy        121 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180

Qy        181 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db        181 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240
Qy        241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300
Db        241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300
Qy        301 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360
Db        301 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360
Qy        361 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP 420
Db        361 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP 420
Qy        421 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 480
Db        421 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 480
Qy        481 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC 540
Db        481 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC 540
Qy        541 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC 600
Db        541 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC 600
Qy        601 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTS------- 653
Db        601 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIISAVVG 660
Qy        654 ------------------------------------------------------------ 653
Db        661 ILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETEL 720
Qy        654 ------------------------------------------------------------ 653
Db        721 RKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSP 780
Qy        654 ------------------------------------------------------------ 653
Db        781 YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVR 840
Qy        654 ------------------------------------------------------------ 653
Db        841 LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT 900
Qy        654 ------------------------------------------------------------ 653
Db        901 HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM 960
Qy        654 ----------------------------QNEDLGPASPLDSTFYRSLLEDDDMGDLVDA 684
Db        961 IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA 1020
Qy        685 EEYLVPQQGFFCPDPAPGAGGMVHHRHR 712
Db       1021 EEYLVPQQGFFCPDPAPGAGGMVHHRHR 1048
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RESULT 9
AAY84780
ID   AAY84780 standard; Protein; 1255 AA.
XX
AC   AAY84780;
XX
DT   08-AUG-2000  (first entry)
XX
DE   Amino acid sequence of the SPLICE erbB-2 receptor protein.
XX
KW   SPLICE erbB-2 receptor protein; cell transformation disorder; cancer;
KW   tumor cell proliferation; tissue degeneration; arthropathy;
KW   bone resorption; inflammatory disease; degenerative disorder;
KW   wound healing.
XX
OS   Homo sapiens.
XX
PN   WO200020579-A1.
XX
PD   13-APR-2000.
XX
PF   01-OCT-1999;   99WO-CA00912.
XX
PR   02-OCT-1998;   98US-0165192.
XX
PA   (UYMC-) UNIV MCMASTER.
XX
PI   Muller WJ,  Siegel PM;
XX
DR   WPI; 2000-303768/26.
DR   N-PSDB; AAA14812.
XX
PT   Nucleic acid encoding an erbB 2 receptor protein designated SPLICE
PT   erbB-2, inhibitors of the protein are useful for treatment of cancer -
XX
PS   Claim 3; Fig 2; 60pp; English.
XX
CC   The present sequence represents a SPLICE erbB-2 receptor protein. The
CC   protein has an in-frame deletion of 16 amino acids, 2 of which are
CC   conserved cysteine residues, compared to the unspliced protein. The
CC   erbB-2 polynucleotide is used to construct probes for detecting
CC   disorders of cell transformation such as cancer. Antibodies to the
CC   protein may be used to detect SPLICE erbB-2 in a sample. Agents
CC   (e.g. antisense oligonucleotides) which inhibit the expression of
CC   SPLICE erbB-2 are useful for reducing tumor cell proliferation and
CC   treating cancer. Substances which stimulate SPLICE erbB-2 are useful
CC   for treating conditions involving damaged cells including conditions
CC   in which degeneration of tissue occurs, such as arthropathy, bone
CC   resorption, inflammatory diseases, degenerative disorders of the
CC   central nervous system and wound healing.
XX
SQ   Sequence   1255 AA;

  Query Match             95.5%;  Score 3776;  DB 21;  Length 1255;
  Best Local Similarity   67.9%;  Pred. No. 6.6e-285;
  Matches  712;  Conservative    0;  Mismatches    0;  Indels  336;  Gaps    1;

Qy          1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60
Db          1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60
Qy         61 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120
Db         61 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120
Qy        121 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180
Db        121 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180
Qy        181 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240
Db        181 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240
Qy        241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300
Db        241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300
Qy        301 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360
Db        301 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360
Qy        361 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP 420
Db        361 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP 420
Qy        421 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 480
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Db        421 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 480

Qy        481 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC 540

Qy        541 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC 600

Qy        601 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTS------- 653
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIISAVVG 660

Qy        654 ------------------------------------------------------------ 653

Db        661 ILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETEL 720

Qy        654 ------------------------------------------------------------ 653

Db        721 RKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSP 780

Qy        654 ------------------------------------------------------------ 653

Db        781 YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVR 840

Qy        654 ------------------------------------------------------------ 653

Db        841 LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT 900

Qy        654 ----------------------------QNEDLGPASPLDSTFYRSLLEDDDMGDLVDA 684
                                           ||||||||||||||||||||||||||||||
Db        901 HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM 960

Qy        654 ----------------------------QNEDLGPASPLDSTFYRSLLEDDDMGDLVDA 684
                                           ||||||||||||||||||||||||||||||
Db        961 IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA 1020

Qy        685 EEYLVPQQGFFCPDPAPGAGGMVHHRHR 712
              ||||||||||||||||||||||||||||
Db       1021 EEYLVPQQGFFCPDPAPGAGGMVHHRHR 1048


RESULT 10
AAY92620
ID   AAY92620 standard; Protein; 1255 AA.
XX
AC   AAY92620;
XX
DT   10-AUG-2000  (first entry)
XX
DE   Human heregulin 2 (Her2).
XX
KW   Heregulin 2; Her2; vaccination; cytotoxic T-lymphocyte immunity;
KW   self-protein; cancer; breast cancer; prostate cancer;
KW   cell-associated peptide antigen; foreign epitope.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Domain          1..173
FT                   /label= N-terminal
FT                   /note= "mature polypeptide"
FT   Region          5..25
FT                   /label= insertion_region
FT                   /note= "suitable for foreign epitope insertion"
FT   Region          59..73
FT                   /label= insertion_region
FT                   /note= "suitable for foreign epitope insertion"
FT   Region          103..117
FT                   /label= insertion_region
FT                   /note= "suitable for foreign epitope insertion"
FT   Region          149..163
FT                   /label= insertion_region
FT                   /note= "suitable for foreign epitope insertion"
FT   Domain          174..323
FT                   /label= Cysteine_rich_domain
FT   Region          210..224
FT                   /label= insertion_region
FT                   /note= "suitable for foreign epitope insertion"
FT   Region          250..264
FT                   /label= insertion_region
FT                   /note= "suitable for foreign epitope insertion"
FT   Domain          324..483
FT                   /label= Ligand_binding_domain
FT   Region          325..339
FT                   /label= insertion_region
FT                   /note= "suitable for foreign epitope insertion"
FT   Region          369..383
FT                   /label= insertion_region
FT                   /note= "suitable for foreign epitope insertion"
FT   Region          465..479
FT                   /label= insertion_region
FT                   /note= "suitable for foreign epitope insertion"
FT   Domain          484..623
FT                   /label= Cysteine_rich_domain
FT   Region          579..593
FT                   /label= insertion_region
FT                   /note= "suitable for foreign epitope insertion"
FT   Domain          624..654
FT                   /label= Transmembrane_domain
FT   Region          632..652
FT                   /label= insertion_region
FT                   /note= "suitable for foreign epitope insertion"
FT   Region          653..667
FT                   /label= insertion_region
FT                   /note= "suitable for foreign epitope insertion"
FT   Domain          655..1010
FT                   /label= Tyrosine_kinase_domain
FT   Region          661..675
FT                   /label= insertion_region
FT                   /note= "suitable for foreign epitope insertion"
FT   Region          695..709
FT                   /label= insertion_region
FT                   /note= "suitable for foreign epitope insertion"
FT   Region          710..730
FT                   /label= insertion_region
FT                   /note= "suitable for foreign epitope insertion"
FT   Domain          1011..1235
FT                   /label= C-terminal_domain
XX
PN   WO200020027-A2.
XX
PD   13-APR-2000.
XX
PF   05-OCT-1999;   99WO-DK00525.
XX
PR   05-OCT-1998;   98DK-0001261.
PR   20-OCT-1998;   98US-0105011.
XX
PA   (MEBI-) M & E BIOTECH AS.
XX
PI   Steinaa L,  Mouritsen S,  Nielsen KG,  Haaning J,  Leach D,  Dalum I;
PI   Gautam A,  Birk P,  Karlsson G;
XX
DR   WPI; 2000-349917/30.
DR   N-PSDB; AAA09455.
XX
PT   Inducing immune responses to weakly immunogenic, tumor associated
PT   peptide antigens for the treatment of breast and prostate cancer
XX
PS   Claim 62; Page 193-198; 220pp; English.
XX
CC   This is the human heregulin 2 (Her2) sequence. Immunogenic analogues of
CC   Her2 can be used in the claimed method as an autovaccine to induce a CTL
CC   response.  Subdominant CTL epitopes, antibody binding regions and
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CC   cysteine residues involved in disulfide bonds are preserved in the
CC   immunogenized forms.  Regions suitable for the insertion of foreign T
CC   helper epitopes were identified (see features table).  The method
CC   is used for inducing immune responses against weakly immunogenic
CC   cell-associated peptide antigens (PA) such as those associated with
CC   cancers (self-proteins), e.g. human prostate specific membrane antigen
CC   (PSM), heregulin 2 (Her2) and/or fibroblast growth factor 8b (FGF8b).
CC   The method comprises effecting simultaneous presentation by antigen
CC   producing cells (APCs) of the animals immune system of: (1) at least 1
CC   CTL (cytotoxic T-lymphocyte) group derived from the PA and/or at least 1
CC   B-cell group derived from the cell-associated PA; and (2) at least 1
CC   first T helper cell group which is foreign to the animal.  Analogues of
CC   human PSM, human Her2 and human/murine FGF8b comprising a substantial
CC   part of all known and predicted CTL and B-cell epitopes of the respective
CC   PA and including at least one foreign T helper epitope are also claimed.
CC   The method is used to treat prostate, prostate/breast or breast cancer
CC   when the PA is human PSM, FGF8b and Her2, respectively.
XX
SQ   Sequence   1255 AA;

  Query Match             95.5%;  Score 3776;  DB 21;  Length 1255;
  Best Local Similarity   67.9%;  Pred. No. 6.6e-285;
  Matches  712;  Conservative    0;  Mismatches    0;  Indels  336;  Gaps    1;

Qy          1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60

Qy         61 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120

Qy        121 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180

Qy        181 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240

Qy        241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300

Qy        301 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360

Qy        361 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP 420

Qy        421 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 480

Qy        481 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC 540

Qy        541 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC 600

Qy        601 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTS------- 653
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVSAVVG 660

Qy        654 ------------------------------------------------------------ 653

Db        661 ILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETEL 720

Qy        654 ------------------------------------------------------------ 653

Db        721 RKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSP 780

Qy        654 ------------------------------------------------------------ 653

Db        781 YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVR 840

Qy        654 ------------------------------------------------------------ 653

Db        841 LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT 900

Qy        654 ------------------------------------------------------------ 653

Db        901 HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM 960

Qy        654 ----------------------------QNEDLGPASPLDSTFYRSLLEDDDMGDLVDA 684
                                           ||||||||||||||||||||||||||||||||
Db        961 IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA 1020

Qy        685 EEYLVPQQGFFCPDPAPGAGGMVHHRHR 712
              ||||||||||||||||||||||||||||
Db       1021 EEYLVPQQGFFCPDPAPGAGGMVHHRHR 1048


RESULT 11
AAE12130
ID   AAE12130 standard; Protein; 1255 AA.
XX
AC   AAE12130;
XX
DT   18-DEC-2001  (first entry)
XX
DE   Human tyrosine kinase-type receptor, HER-2.
XX
KW   Therapeutic compound; major histocompatibility complex; vaccine;
KW   antigenic peptide; MHC; immunoregulatory; immune response; HER-2;
KW   adoptive immunotherapy; anti-cancer; breast cancer antigen; APC;
KW   antigen presenting cell; human; tyrosine kinase-type receptor.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          774..782
FT                   /note= "Antigenic epitope"
XX
PN   WO200168677-A2.
XX
PD   20-SEP-2001.
XX
PF   16-MAR-2001; 2001WO-US40328.
XX
PR   16-MAR-2000; 2000US-0527487.
XX
PA   (GENZ ) GENZYME CORP.
XX
PI   Nicolette CA;
XX
DR   WPI; 2001-616284/71.
DR   N-PSDB; AAD19731.
XX
PT   Novel synthetic therapeutic compound for inducing immune response and
PT   for use in adoptive immunotherapy, has enhanced binding to major
PT   histocompatibility molecules and enhanced immunoregulatory properties
PT   -
XX
PS   Claim 4; Page 63-67; 69pp; English.
XX
CC   The invention relates to synthetic therapeutic compounds (antigenic
CC   peptides) with enhanced binding to major histocompatibility complex
CC   (MHC) molecules and enhanced immunoregulatory properties relative
CC   to their natural counterparts. Compounds of the invention are useful
CC   for inducing an immune response in a subject and for use in adoptive
CC   immunotherapy. They are useful as components of anti-cancer vaccines
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CC   and to expand immune effector cells that are specific for cancers
CC   characterised by expression of the breast cancer antigen, HER-2.
CC   Polynucleotides that encode peptides of the invention are useful as
CC   hybridisation probes and as primers for the detection of genes of gene
CC   transcripts that are expressed in antigen presenting cells (APCs), to
CC   confirm transduction of polynucleotides into host cells. The present
CC   sequence is human tyrosine kinase-type receptor, HER-2. Compounds
CC   of the invention are designed based on the HER-2 antigenic peptide
CC   (774-782).
XX
SQ   Sequence   1255 AA;

  Query Match             95.5%;  Score 3776;  DB 22;  Length 1255;
  Best Local Similarity   67.9%;  Pred. No. 6.6e-285;
  Matches  712;  Conservative    0;  Mismatches    0;  Indels  336;  Gaps    1;

Qy          1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60

Qy         61 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120

Qy        121 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180

Qy        181 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240

Qy        241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300

Qy        301 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360

Qy        361 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP 420

Qy        421 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 480

Qy        481 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC 540

Qy        541 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC 600

Qy        601 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTS------- 653
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVSAVVG 660

Qy        654 ------------------------------------------------------------ 653

Db        661 ILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETEL 720

Qy        654 ------------------------------------------------------------ 653

Db        721 RKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSP 780

Qy        654 ------------------------------------------------------------ 653

Db        781 YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVR 840

Qy        654 ------------------------------------------------------------ 653

Db        841 LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT 900

Qy        654 ------------------------------------------------------------ 653

Db        901 HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM 960

Qy        654 ----------------------------QNEDLGPASPLDSTFYRSLLEDDDMGDLVDA 684
                                           ||||||||||||||||||||||||||||||
Db        961 IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA 1020

Qy        685 EEYLVPQQGFFCPDPAPGAGGMVHHRHR 712
              ||||||||||||||||||||||||||||
Db       1021 EEYLVPQQGFFCPDPAPGAGGMVHHRHR 1048


RESULT 12
AAB85458
ID   AAB85458 standard; Protein; 1255 AA.
XX
AC   AAB85458;
XX
DT   25-SEP-2001  (first entry)
XX
DE   Human HER-2/neu protein.
XX
KW   Antigen-presenting cell; immunogenic; immune response; HER-2/neu;
KW   oncogene; cancer; cytostatic; vaccine; p185; c-erbB2.
XX
OS   Homo sapiens.
XX
PN   WO200153463-A2.
XX
PD   26-JUL-2001.
XX
PF   19-JAN-2001; 2001WO-US01850.
XX
PR   21-JAN-2000; 2000US-0177545.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Cheever MA,  Hand-Zimmermann S;
XX
DR   WPI; 2001-476112/51.
DR   N-PSDB; AAH23392.
XX
PT   New antigen-presenting cells, useful as vaccines for eliciting or
PT   enhancing an immune response to HER-2/neu protein, particularly useful
PT   for treating or preventing cancer, e.g. breast cancer  -
XX
PS   Claim 2; Page 41-46; 49pp; English.
XX
CC   The invention provides an isolated antigen-presenting cell, which
CC   expresses at least an immunogenic portion of a polypeptide that produces
CC   an immune response to HER-2/neu protein. The antigen-presenting cells are
CC   useful as vaccines for eliciting or enhancing an immune response to
CC   HER-2/neu protein, particularly in treating or preventing malignancies in
CC   which the HER-2/neu oncogene is associated. Specifically, these are
CC   useful for treating or preventing cancer, e.g. breast cancer, ovarian,
CC   colon, lung or prostate cancers. The present sequence represents
CC   the human HER-2/neu protein (also known as p185 or c-erbB2).
XX
SQ   Sequence   1255 AA;

  Query Match             95.5%;  Score 3776;  DB 22;  Length 1255;
  Best Local Similarity   67.9%;  Pred. No. 6.6e-285;
  Matches  712;  Conservative    0;  Mismatches    0;  Indels  336;  Gaps    1;

Qy          1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60

Qy         61 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120

Qy         121 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180

Qy         181 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240

Qy         241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300

Qy         301 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360

Qy         361 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP 420
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP 420

Qy         421 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 480
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 480

Qy         481 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC 540
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC 540

Qy         541 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC 600
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC 600

Qy         601 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTS------- 653
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIISAVVG 660

Qy         654 ------------------------------------------------------------ 653

Db         661 ILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETEL 720

Qy         654 ------------------------------------------------------------ 653

Db         721 RKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSP 780

Qy         654 ------------------------------------------------------------ 653

Db         781 YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVR 840

Qy         654 ------------------------------------------------------------ 653

Db         841 LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT 900

Qy         654 ------------------------------------------------------------ 653

Db         901 HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM 960

Qy         654 ----------------------------QNEDLGPASPLDSTFYRSLLEDDDMGDLVDA 684
                                            ||||||||||||||||||||||||||||||||
Db         961 IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA 1020

Qy         685 EEYLVPQQGFFCPDPAPGAGGMVHHRHR 712
                 ||||||||||||||||||||||||||||
Db        1021 EEYLVPQQGFFCPDPAPGAGGMVHHRHR 1048
```

RESULT 13
AAG88267
ID AAG88267 standard; Protein; 1255 AA.
XX
AC AAG88267;
XX
DT 11-SEP-2001 (first entry)
XX
DE HER2/neu amino acid sequence.
XX
KW Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;
KW immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;
KW tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.
XX
OS Homo sapiens.
XX
PN WO200141787-A1.
XX
PD 14-JUN-2001.
XX
PF 11-DEC-2000; 2000WO-US33591.
XX
PR 10-DEC-1999; 99US-0458299.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;
PI Keogh E;
XX
DR WPI; 2001-374995/39.
XX
PT An isolated prepared HER2/neu epitope useful in a vaccine for inducing
PT cellular immune responses for the prevention and treatment of cancer -
XX
PS Disclosure; Page 15; 199pp; English.
XX
CC The present invention describes isolated prepared HER2/neu epitopes (I).
CC Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is
CC culture in vitro and binds to a complex of an epitope (I), bound to a
CC human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)
CC and a second epitope and the peptide is less than 50 contiguous amino
CC acids that have 100% identity with a native peptide sequence of HER2/neu;
CC (3) a vaccine composition (III) comprising (II) and a pharmaceutical
CC excipient; (4) an isolated nucleic acid encoding a peptide comprising
CC (I); and (5) an isolated nucleic acid encoding (II). (I) has cytostatic
CC and immunostimulant activities, and can be used in vaccines. (I), (II)
CC and (III) are useful for inducing cellular immune responses for the
CC prevention and treatment of cancer. (I) and (II) are useful for
CC monitoring or evaluating an immune response to a tumour-associated
CC antigen when incubated with a T lymphocyte sample form a patient and
CC detecting the presence of bound T lymphocyte to (I) or (II). Epitope
CC based vaccines mean that immunosuppressive epitopes that may be present
CC in whole antigens may be avoided. Selected epitopes may be combined to
CC enhance immunogenicity. The possible pathological side effects caused by
CC infectious agents or whole protein antigen is eliminated. The vaccine
CC provides the ability to direct and focus an immune response to multiple
CC selected antigens from the same pathogen. Epitope-based anti-tumour
CC vaccines provides the opportunity to combine epitopes derived from
CC multiple tumour-associated molecules addressing the problem of tumour-
CC tumour variability and reducing the likelihood of tumour escape due to
CC antigen loss. AAG88266 to AAG89121 represent amino acid sequences used in
CC the exemplification of the present invention.
XX
SQ Sequence 1255 AA;

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  Query Match             95.5%;  Score 3776;  DB 22;  Length 1255;
  Best Local Similarity   67.9%;  Pred. No. 6.6e-285;
  Matches  712;  Conservative    0;  Mismatches    0;  Indels  336;  Gaps    1;

Qy           1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60

Qy          61 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120

Qy         121 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180
```

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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180

Qy        181 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240

Qy        241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300

Qy        301 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360

Qy        361 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP 420

Qy        421 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 480

Qy        481 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC 540

Qy        541 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC 600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC 600

Qy        601 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTS------- 653
                ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIISAVVG 660

Qy        654 ---------------------------------------------------------- 653

Db        661 ILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETEL 720

Qy        654 ---------------------------------------------------------- 653

Db        721 RKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSP 780

Qy        654 ---------------------------------------------------------- 653

Db        781 YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVR 840

Qy        654 ---------------------------------------------------------- 653

Db        841 LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT 900

Qy        654 ---------------------------------------------------------- 653

Db        901 HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM 960

Qy        654 ----------------------------QNEDLGPASPLDSTFYRSLLEDDDMGDLVDA 684
                                           ||||||||||||||||||||||||||||||
Db        961 IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA 1020

Qy        685 EEYLVPQQGFFCPDPAPGAGGMVHHRHR 712
                ||||||||||||||||||||||||||||
Db       1021 EEYLVPQQGFFCPDPAPGAGGMVHHRHR 1048


RESULT 14
AAB60167
ID   AAB60167 standard; Protein; 1255 AA.
XX
AC   AAB60167;
XX
DT   03-APR-2001  (first entry)
XX
DE   HER2 transgene plasmid construct encoded protein.
XX
KW   Human; HER2; ErbB2 receptor; p185neu; maytansinoid conjugate; cancer;
KW   antibody.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200100244-A2.
XX
PD   04-JAN-2001.
XX
PF   23-JUN-2000; 2000WO-US17229.
XX
PR   25-JUN-1999;   99US-0141316.
PR   16-MAR-2000; 2000US-0189844.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Erickson S,  Schwall R;
XX
DR   WPI; 2001-061962/07.
DR   N-PSDB; AAF24297.
XX
PT   Treating tumors, particularly breast cancers, which overexpress an ErbB
PT   receptor and does not respond to an anti-ErbB antibody, comprises
PT   conjugating the antibody to a maytansinoid -
XX
PS   Example 3; Fig 4; 92pp; English.
XX
CC   The present invention provides a method of treating cancer by
CC   administering a conjugate of anti-ErbB antibody with a maytansinoid. In
CC   particular, the antibody is directed against ErbB2 (also known as HER2
CC   and p185neu). The method is particularly useful in the treatment of
CC   breast, ovarian, stomach, endometrial, salivary gland, lung, kidney,
CC   colon, colorectal, thyroid, pancreatic, prostate and bladder cancers.
XX
SQ   Sequence   1255 AA;

  Query Match             95.5%;  Score 3776;  DB 22;  Length 1255;
  Best Local Similarity   67.9%;  Pred. No. 6.6e-285;
  Matches  712;  Conservative    0;  Mismatches    0;  Indels  336;  Gaps    1;

Qy          1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60

Qy         61 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120

Qy        121 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180

Qy        181 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240

Qy        241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300

Qy        301 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360

Qy        361 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP 420

Qy        421 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 480
```

```
Qy        481 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC 540

Qy        541 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC 600

Qy        601 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTS------- 653
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVSAVVG 660

Qy        654 ------------------------------------------------------------ 653

Db        661 ILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETEL 720

Qy        654 ------------------------------------------------------------ 653

Db        721 RKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSP 780

Qy        654 ------------------------------------------------------------ 653

Db        781 YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVR 840

Qy        654 ------------------------------------------------------------ 653

Db        841 LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT 900

Qy        654 ------------------------------------------------------------ 653

Db        901 HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM 960

Qy        654 ---------------------------QNEDLGPASPLDSTFYRSLLEDDDMGDLVDA 684
                                          ||||||||||||||||||||||||||||||
Db        961 IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA 1020

Qy        685 EEYLVPQQGFFCPDPAPGAGGMVHHRHR 712
              ||||||||||||||||||||||||||||
Db       1021 EEYLVPQQGFFCPDPAPGAGGMVHHRHR 1048
```

```
RESULT 15
AAE26349
ID   AAE26349 standard; Protein; 1255 AA.
XX
AC   AAE26349;
XX
DT   13-DEC-2002  (first entry)
XX
DE   Human HER-2 protein.
XX
KW   Transgenic animal; transgenic; mammary gland cell; HER2; tumour;
KW   cancer; therapy; apoptosis; cytostatic; human.
XX
OS   Homo sapiens.
XX
PN   US2002035736-A1.
XX
PD   21-MAR-2002.
XX
PF   16-MAR-2001; 2001US-0811115.
XX
PR   16-MAR-2000; 2000US-189844P.
XX
PA   (ERIC/) ERICKSON S.
PA   (KING/) KING K.
PA   (SCHW/) SCHWALL R.
XX
PI   Erickson S,  King K,  Schwall R;
XX
DR   WPI; 2002-401155/43.
DR   N-PSDB; AAD43934, AAD43935.
XX
PT   New transgenic non-human mammal that produces detectable levels of a
PT   native human HER2 protein in its mammary gland cells, useful as tumor
PT   models for testing HER2-directed cancer therapies, and for identifying
PT   anticancer agents -
XX
PS   Example 2; Page 26-29; 83pp; English.
XX
CC   The invention relates to a transgenic non-human mammal that produces in
CC   its mammary gland cells detectable levels of a native human HER2 protein
CC   or its fragment. The transgenic animals are useful as tumour models for
CC   testing HER2-directed cancer therapies, and for identifying anticancer
CC   agents. The animals may also be used as source of cells which can be
CC   immortalised in culture, in screening for compounds that have potential
CC   as prophylactic or therapeutic treatments of diseases or disorders
CC   involving expression of HER2. The anti-cancer molecules are useful for
CC   inducing apoptosis or cell death of cancer cells. The present sequence
CC   is human HER-2 protein.
XX
SQ   Sequence   1255 AA;
```

```
  Query Match             95.5%;  Score 3776;  DB 23;  Length 1255;
  Best Local Similarity   67.9%;  Pred. No. 6.6e-285;
  Matches  712;  Conservative    0;  Mismatches    0;  Indels  336;  Gaps    1;

Qy          1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60

Qy         61 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120

Qy        121 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180

Qy        181 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240

Qy        241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300

Qy        301 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360

Qy        361 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP 420

Qy        421 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 480

Qy        481 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC 540

Qy        541 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC 600

Qy        601 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTS------- 653
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVSAVVG 660

Qy        654 ------------------------------------------------------------ 653

Db        661 ILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETEL 720
```

```
Qy        654 ------------------------------------------------------------ 653

Db        721 RKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSP 780

Qy        654 ------------------------------------------------------------ 653

Db        781 YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVR 840

Qy        654 ------------------------------------------------------------ 653

Db        841 LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT 900

Qy        654 ------------------------------------------------------------ 653

Db        901 HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM 960

Qy        654 ----------------------------QNEDLGPASPLDSTFYRSLLEDDDMGDLVDA 684
                                           ||||||||||||||||||||||||||||||
Db        961 IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA 1020

Qy        685 EEYLVPQQGFFCPDPAPGAGGMVHHRHR 712
              ||||||||||||||||||||||||||||
Db       1021 EEYLVPQQGFFCPDPAPGAGGMVHHRHR 1048
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Search completed: December 5, 2003, 14:33:25
Job time : 46.3599 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 5, 2003, 14:26:38 ; Search time 45.6401 Seconds
(without alignments)
3196.087 Million cell updates/sec

Title: US-09-854-356-6
Perfect score: 5078
Sequence: 1 MELAALCRWGLLLALLPPGA.....TFKGTPTAENPEYLGLDVPV 919

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5078	100.0	919	21	AAB21203	Human HER-2/neu fu
2	5078	100.0	919	23	AAM51148	Her-2/neu extracel
3	4900	96.5	1255	17	AAW01111	HER-2/neu protein.
4	4900	96.5	1255	20	AAW92406	Human HER-2/neu on
5	4900	96.5	1255	21	AAB21198	Human HER-2/neu pr
6	4900	96.5	1255	21	AAY84780	Amino acid sequenc
7	4900	96.5	1255	22	AAB85458	Human HER-2/neu pr
8	4900	96.5	1255	22	AAG88267	HER2/neu amino aci
9	4900	96.5	1255	23	AAE24067	Human Her-2 protei
10	4900	96.5	1255	23	AAE20479	Human Her-2/neu pr
11	4900	96.5	1255	23	AAM51143	Human Her-2/neu on
12	4900	96.5	1255	23	AAU77114	Human Her-2/neu po
13	4892	96.3	1255	21	AAY92620	Human heregulin 2
14	4892	96.3	1255	22	AAE12130	Human tyrosine kin
15	4892	96.3	1255	22	AAB60167	HER2 transgene pla
16	4892	96.3	1255	23	AAE26349	Human HER-2 protei
17	4892	96.3	1255	23	AAE26366	Human Her2 antigen
18	4892	96.3	1255	23	AAU74545	Human HER2 (ErbB2)
19	4892	96.3	1255	24	ABR47447	Breast cancer asso
20	4892	96.3	1255	24	ABP74708	Human Her2/Neu pro
21	4857	95.6	1433	14	AAR39568	Sequence of c-erbB
22	4722	93.0	1223	23	AAU98923	Human breast cance
23	4583	90.3	1200	21	AAB21208	Human HER-2/neu pr
24	4309.5	84.9	920	23	AAM51152	Mouse Her-2/neu ex
25	4309.5	84.9	926	23	AAM51153	Mouse Her-2/neu ex
26	4138.5	81.5	1256	21	AAB21199	Rat HER-2/neu prot
27	4138.5	81.5	1256	23	AAM51144	Rat Her-2/neu onco
28	4125.5	81.2	1256	21	AAB21206	Mouse Her-2/neu pr
29	4125.5	81.2	1256	22	AAG62860	Amino acid sequenc
30	4125.5	81.2	1256	23	AAM51151	Mouse Her-2/neu on
31	3954	77.9	712	21	AAB21204	Human HER-2/neu fu
32	3954	77.9	712	23	AAM51149	Her-2/neu extracel
33	3632	71.5	782	18	AAW19764	Her2-GM-CSF immuno
34	3628	71.4	653	21	AAB21200	Extracellular HER-
35	3628	71.4	653	23	AAM51145	Human Her-2/neu on
36	3590	70.7	645	22	AAB60408	Human ErbB2 oncopr
37	3590	70.7	645	22	AAB61593	Human ErbB2 extrac
38	3590	70.7	645	23	ABG70753	Human HER2 recepto
39	3525	69.4	951	21	AAY44993	DC8scFv-erbB2EC fu
40	3422	67.4	624	11	AAR08222	Extracellular port
41	3110.5	61.3	654	21	AAB21205	Rat HER-2/neu prot
42	3110.5	61.3	654	23	AAM51150	Rat Her-2/neu onco
43	2585	50.9	564	22	AAE13110	Human HER500 fusio
44	2585	50.9	697	22	AAE13111	Human HER500-rGM-C
45	2573.5	50.7	555	22	AAE13108	Human HER500 fusio

ALIGNMENTS

RESULT 1
AAB21203
ID AAB21203 standard; protein; 919 AA.
XX
AC AAB21203;
XX
DT 12-JAN-2001 (first entry)
XX
DE Human HER-2/neu fusion protein.
XX
KW Human; HER-2/neu; oncogene; tyrosine kinase; cytostatic; vaccine;
KW breast cancer; prostate cancer; ovarian cancer; lung cancer;
KW colon cancer; fusion protein.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200044899-A1.
XX
PD 03-AUG-2000.
XX
PF 28-JAN-2000; 2000WO-US02164.
XX
PR 29-JAN-1999; 99US-0117976.
XX
PA (CORI-) GORIXA CORP.
PA (SMIK) SMITHKLINE BEECHAM.
XX
PI Cheever MA, Gheysen D;
XX
DR WPI; 2000-505976/45.
XX

```
PT   HER-2/neu extracellular domain/phosphorylation domain fusion proteins
PT   useful for vaccinating against breast, ovarian, colon, lung and
PT   prostate cancers -
XX
PS   Claim 2; Fig 12; 128pp; English.
XX
CC   The present sequence is a fusion protein comprising the extracellular
CC   domain and the phosphorylation domain of the human HER-2/neu protein.
CC   HER-2/neu is a member of the tyrosine kinase family of receptor-like
CC   glycoproteins and shows homology to the epidermal growth factor receptor
CC   (EGFR). It probably plays a part in cell growth and/or differentiation.
CC   The HER-2/neu gene is an oncogene. HER-2/neu fusion proteins may be used
CC   to treat or prevent cancer by eliciting or enhancing an immune response
CC   to the HER-2/neu protein. They may be used to treat malignancies such as
CC   breast, ovarian, colon, lung and prostate cancers, and may be used as an
CC   antigen to vaccinate against these neoplasias.
XX
SQ   Sequence   919 AA;

  Query Match            100.0%;  Score 5078;  DB 21;  Length 919;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  919;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60

Qy         61 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120

Qy        121 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180

Qy        181 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240

Qy        241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300

Qy        301 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360

Qy        361 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP 420

Qy        421 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 480

Qy        481 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC 540

Qy        541 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC 600

Qy        601 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSQNEDLGP 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSQNEDLGP 660

Qy        661 ASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGG 720

Qy        721 GDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDP 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDP 780

Qy        781 TVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERPKTLSPG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERPKTLSPG 840

Qy        841 KNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPST 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 KNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPST 900

Qy        901 FKGTPTAENPEYLGLDVPV 919
              |||||||||||||||||||
Db        901 FKGTPTAENPEYLGLDVPV 919


RESULT 2
AAM51148
ID   AAM51148 standard; Protein; 919 AA.
XX
AC   AAM51148;
XX
DT   17-JUN-2002  (first entry)
XX
DE   Her-2/neu extracellular domain-phosphorylation domain fusion.
XX
KW   Her-2/neu; oncogene; cancer; tumour; vaccine; human; p185;
KW   tyrosine kinase; receptor; c-erbB2; gene therapy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Domain          1..653
FT                   /note= "extracellular domain"
FT   Domain          654..919
FT                   /note= "phosphorylation domain"
XX
PN   WO200212341-A2.
XX
PD   14-FEB-2002.
XX
PF   03-AUG-2001; 2001WO-US24283.
XX
PR   03-AUG-2000; 2000US-0632507.
XX
PA   (CORI-) CORIXA CORP.
PA   (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI   Cheever MA,  Gheysen D;
XX
DR   WPI; 2002-241743/29.
XX
PT   Her-2/neu fusion protein for treating or preventing cancer by eliciting
PT   or enhancing an immune response to the protein, has Her-2/neu
PT   extracellular domain fused to Her-2/neu intracellular or
PT   phosphorylation domain  -
XX
PS   Claim 2; Fig 12; 141pp; English.
XX
CC   The present sequence is that of a fusion protein between the
CC   extracellular domain and phosphorylation domain of human Her-2/neu
CC   (see AAM51143), an oncogenic self-protein and target for anti-cancer
CC   vaccines.  The fusion protein can be obtained by recombinant DNA
CC   methods.  Her-2/neu overexpression correlates with a poor prognosis
CC   in breast and ovarian cancers.  The invention provides Her-2/neu
CC   fusion proteins, nucleic acids encoding them, viral vectors, and
CC   vaccines comprising the fusion proteins or nucleic acid molecules.
CC   In preferred fusion proteins, the extracellular domain of a
CC   Her-2/neu protein is fused to a Her-2/neu intracellular domain or
CC   phosphorylation domain (or its DeltaPD fragment).  An immune
CC   response to Her-2/neu protein is elicited or enhanced by
CC   administering the fusion protein in the form of a vaccine, or by
CC   transfecting cells of an animal ex vivo with a nucleic acid
CC   encoding the fusion protein, and delivering the transfected cells
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CC   to the animal.  The fusion proteins, nucleic acids, and isolated
CC   specific T-cells are useful for inhibiting the development of a
CC   cancer, especially breast, ovarian, colon, lung or prostate cancer
CC   in a patient.  T cells that specifically react with a Her-2/neu
CC   fusion protein can be used to remove tumour cells from a sample in
CC   order to inhibit the development of cancer in a patient.
XX
SQ   Sequence   919 AA;

  Query Match            100.0%;  Score 5078;  DB 23;  Length 919;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  919;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60

Qy         61 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120

Qy        121 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180

Qy        181 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240

Qy        241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300

Qy        301 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360

Qy        361 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP 420

Qy        421 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 480

Qy        481 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC 540

Qy        541 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC 600

Qy        601 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSQNEDLGP 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSQNEDLGP 660

Qy        661 ASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGG 720

Qy        721 GDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDP 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDP 780

Qy        781 TVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERPKTLSPG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERPKTLSPG 840

Qy        841 KNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPST 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 KNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPST 900
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Qy        901 FKGTPTAENPEYLGLDVPV 919
              |||||||||||||||||||
Db        901 FKGTPTAENPEYLGLDVPV 919


RESULT 3
AAW01111
ID   AAW01111 standard; Protein; 1255 AA.
XX
AC   AAW01111;
XX
DT   01-JAN-1997  (first entry)
XX
DE   HER-2/neu protein.
XX
KW   HER-2/neu; c-erbB1; p185; oncogene; tyrosine protein kinase;
KW   breast cancer; ovary cancer; colon cancer; lung cancer;
KW   prostate cancer; immunisation; tumour; vaccine; vector.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Domain          676..1255
FT                   /label= Intracellular_domain
FT                   /note= "claimed domain, useful for immunisation"
XX
PN   WO9630514-A1.
XX
PD   03-OCT-1996.
XX
PF   28-MAR-1996;   96WO-US01689.
XX
PR   31-MAR-1995;   95US-0414417.
XX
PA   (UNIW ) UNIV WASHINGTON.
XX
PI   Cheever MA,  Disis ML;
XX
DR   WPI; 1996-455361/45.
DR   N-PSDB; AAT40739.
XX
PT   DNA encoding HER-2-neu poly:peptide(s) - used for prevention or
PT   treatment of malignancies with which the HER-2/neu oncogene is
PT   associated
XX
PS   Claim 2; Page 56-61; 71pp; English.
XX
CC   Human HER-2/neu protein (AAW01111), also called p185 or c-erbB2, is
CC   the product of the HER-2/neo oncogene (see also AAT40739).  The
CC   protein is over-expressed in various cancers, including breast,
CC   ovarian, colon, lung and prostate.  The intracellular domain of the
CC   protein can be used to immunise an animal against a malignancy with
CC   which the oncogene is associated.  The polypeptide can be produced
CC   in transformed host cells for use in immunisation.  Alternatively,
CC   animal cells are transfected in vivo or ex vivo with a viral vector
CC   that directs expression of the polypeptide.
XX
SQ   Sequence   1255 AA;

  Query Match            96.5%;  Score 4900;  DB 17;  Length 1255;
  Best Local Similarity  73.2%;  Pred. No. 0;
  Matches  919;  Conservative    0;  Mismatches    0;  Indels  336;  Gaps    1;

Qy          1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60

Qy         61 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120

Qy        121 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        121 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180

Qy        181 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240

Qy        241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300

Qy        301 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360

Qy        361 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP 420

Qy        421 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 480

Qy        481 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC 540

Qy        541 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC 600

Qy        601 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTS------- 653
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIISAVVG 660

Qy        654 ---------------------------------------------------------- 653

Db        661 ILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETEL 720

Qy        654 ---------------------------------------------------------- 653

Db        721 RKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSP 780

Qy        654 ---------------------------------------------------------- 653

Db        781 YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVR 840

Qy        654 ---------------------------------------------------------- 653

Db        841 LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT 900

Qy        654 ---------------------------------------------------------- 653

Db        901 HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM 960

Qy        654 ----------------------------QNEDLGPASPLDSTFYRSLLEDDDMGDLVDA 684
                                           ||||||||||||||||||||||||||||||
Db        961 IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA 1020

Qy        685 EEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG 744
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 EEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG 1080

Qy        745 AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV 804
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV 1140

Qy        805 NQPDVRPQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ 864
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 NQPDVRPQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ 1200

Qy        865 GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 919
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1255
```

```
RESULT 4
AAW92406
ID   AAW92406 standard; Protein; 1255 AA.
XX
AC   AAW92406;
XX
DT   21-APR-1999  (first entry)
XX
DE   Human HER-2/neu oncogene protein.
XX
KW   HER-2/neu; oncogene; immune response; T cell; B cell; immunisation;
KW   malignancy; treatment; tumour.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          676..1255
FT                   /note= "region which elicits immune response"
XX
PN   US5869445-A.
XX
PD   09-FEB-1999.
XX
PF   01-APR-1996;   96US-0625101.
XX
PR   01-APR-1996;   96US-0625101.
PR   17-MAR-1993;   93US-0033644.
PR   12-AUG-1993;   93US-0106112.
PR   31-MAR-1995;   95US-0414417.
XX
PA   (UNIW ) UNIV WASHINGTON.
XX
PI   Cheever MA,  Disis ML;
XX
DR   WPI; 1999-152835/13.
DR   N-PSDB; AAX01912.
XX
PT   Use of HER-2/neu polypeptides - for eliciting an immune response to
PT   an HER-2/neu associated malignancy, particularly for treating or
PT   preventing tumours
XX
PS   Claim 3; Column 31-38; 26pp; English.
XX
CC   This sequence represents the human HER-2/neu oncogene protein. A fragment
CC   of this protein is used in a method for eliciting or enhancing an immune
CC   response to HER-2/neu protein. The polypeptide can stimulate T cells and
CC   B cells to produce an immune response to the HER-2/neu protein. The
CC   method can be used for immunisation against a malignancy in which the
CC   HER-2/neu oncogene is associated and in the treatment of an existing
CC   tumour, or to prevent tumour occurrence or reoccurrence.
XX
SQ   Sequence   1255 AA;

  Query Match             96.5%;  Score 4900;  DB 20;  Length 1255;
  Best Local Similarity   73.2%;  Pred. No. 0;
  Matches  919;  Conservative    0;  Mismatches    0;  Indels  336;  Gaps    1;

Qy          1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60

Qy         61 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120

Qy        121 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180

Qy        181 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        181 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240
Qy        241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300
Db        241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300
Qy        301 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360
Db        301 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360
Qy        361 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP 420
Db        361 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP 420
Qy        421 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 480
Db        421 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 480
Qy        481 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC 540
Db        481 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC 540
Qy        541 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC 600
Db        541 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC 600
Qy        601 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTS------- 653
Db        601 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIISAVVG 660
Qy        654 ---------------------------------------------------------- 653
Db        661 ILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETEL 720
Qy        654 ---------------------------------------------------------- 653
Db        721 RKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSP 780
Qy        654 ---------------------------------------------------------- 653
Db        781 YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVR 840
Qy        654 ---------------------------------------------------------- 653
Db        841 LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT 900
Qy        654 ---------------------------------------------------------- 653
Db        901 HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM 960
Qy        654 ----------------------------QNEDLGPASPLDSTFYRSLLEDDDMGDLVDA 684
Db        961 IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA 1020
Qy        685 EEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG 744
Db       1021 EEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG 1080
Qy        745 AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV 804
Db       1081 AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV 1140
Qy        805 NQPDVRPQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ 864
Db       1141 NQPDVRPQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ 1200
Qy        865 GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 919
Db       1201 GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1255
```

RESULT 5
AAB21198

```
ID   AAB21198 standard; protein; 1255 AA.
XX
AC   AAB21198;
XX
DT   12-JAN-2001  (first entry)
XX
DE   Human HER-2/neu protein.
XX
KW   Human; HER-2/neu; oncogene; tyrosine kinase; cytostatic; vaccine;
KW   breast cancer; prostate cancer; ovarian cancer; lung cancer;
KW   colon cancer.
XX
OS   Homo sapiens.
XX
PN   WO200044899-A1.
XX
PD   03-AUG-2000.
XX
PF   28-JAN-2000; 2000WO-US02164.
XX
PR   29-JAN-1999;   99US-0117976.
XX
PA   (CORI-) CORIXA CORP.
PA   (SMIK ) SMITHKLINE BEECHAM.
XX
PI   Cheever MA,  Gheysen D;
XX
DR   WPI; 2000-505976/45.
DR   N-PSDB; AAA89736.
XX
PT   HER-2/neu extracellular domain/phosphorylation domain fusion proteins
PT   useful for vaccinating against breast, ovarian, colon, lung and
PT   prostate cancers -
XX
PS   Claim 52; Fig 7; 128pp; English.
XX
CC   The present sequence is the human HER-2/neu protein. It is a member of
CC   the tyrosine kinase family of receptor-like glycoproteins and shows
CC   homology to the epidermal growth factor receptor (EGFR). It probably
CC   plays a part in cell growth and/or differentiation. The HER-2/neu
CC   gene is an oncogene. An HER-2/neu fusion protein comprising a
CC   HER-2/neu extracellular domain fused to a HER-2/neu phosphorylation
CC   domain may be used to treat or prevent cancer by eliciting or
CC   enhancing an immune response to the HER-2/neu protein. It may be used
CC   to treat malignancies such as breast, ovarian, colon, lung and
CC   prostate cancers, and may be used as an antigen to vaccinate against
CC   these neoplasias.
XX
SQ   Sequence   1255 AA;

  Query Match             96.5%;  Score 4900;  DB 21;  Length 1255;
  Best Local Similarity   73.2%;  Pred. No. 0;
  Matches  919;  Conservative    0;  Mismatches    0;  Indels  336;  Gaps    1;

Qy          1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60
Db          1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60
Qy         61 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120
Db         61 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120
Qy        121 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180
Db        121 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180
Qy        181 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240
Db        181 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240
Qy        241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300
Db        241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300
```

```
Qy        301 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360

Qy        361 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP 420

Qy        421 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 480

Qy        481 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC 540

Qy        541 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC 600

Qy        601 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTS------- 653
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIISAVVG 660

Qy        654 ------------------------------------------------------------ 653

Db        661 ILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETEL 720

Qy        654 ------------------------------------------------------------ 653

Db        721 RKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSP 780

Qy        654 ------------------------------------------------------------ 653

Db        781 YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVR 840

Qy        654 ------------------------------------------------------------ 653

Db        841 LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT 900

Qy        654 ------------------------------------------------------------ 653

Db        901 HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM 960

Qy        654 ----------------------------QNEDLGPASPLDSTFYRSLLEDDDMGDLVDA 684
                                           ||||||||||||||||||||||||||||||
Db        961 IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA 1020

Qy        685 EEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG 744
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 EEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG 1080

Qy        745 AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV 804
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV 1140

Qy        805 NQPDVRPQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ 864
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 NQPDVRPQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ 1200

Qy        865 GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 919
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1255
```

```
RESULT 6
AAY84780
ID   AAY84780 standard; Protein; 1255 AA.
XX
AC   AAY84780;
XX
DT   08-AUG-2000  (first entry)
XX
DE   Amino acid sequence of the SPLICE erbB-2 receptor protein.
XX
KW   SPLICE erbB-2 receptor protein; cell transformation disorder; cancer;
KW   tumor cell proliferation; tissue degeneration; arthropathy;
KW   bone resorption; inflammatory disease; degenerative disorder;
KW   wound healing.
XX
OS   Homo sapiens.
XX
PN   WO200020579-A1.
XX
PD   13-APR-2000.
XX
PF   01-OCT-1999;   99WO-CA00912.
XX
PR   02-OCT-1998;   98US-0165192.
XX
PA   (UYMC-) UNIV MCMASTER.
XX
PI   Muller WJ,  Siegel PM;
XX
DR   WPI; 2000-303768/26.
DR   N-PSDB; AAA14812.
XX
PT   Nucleic acid encoding an erbB 2 receptor protein designated SPLICE
PT   erbB-2, inhibitors of the protein are useful for treatment of cancer -
XX
PS   Claim 3; Fig 2; 60pp; English.
XX
CC   The present sequence represents a SPLICE erbB-2 receptor protein. The
CC   protein has an in-frame deletion of 16 amino acids, 2 of which are
CC   conserved cysteine residues, compared to the unspliced protein. The
CC   erbB-2 polynucleotide is used to construct probes for detecting
CC   disorders of cell transformation such as cancer. Antibodies to the
CC   protein may be used to detect SPLICE erbB-2 in a sample. Agents
CC   (e.g. antisense oligonucleotides) which inhibit the expression of
CC   SPLICE erbB-2 are useful for reducing tumor cell proliferation and
CC   treating cancer. Substances which stimulate SPLICE erbB-2 are useful
CC   for treating conditions involving damaged cells including conditions
CC   in which degeneration of tissue occurs, such as arthropathy, bone
CC   resorption, inflammatory diseases, degenerative disorders of the
CC   central nervous system and wound healing.
XX
SQ   Sequence   1255 AA;

  Query Match             96.5%;  Score 4900;  DB 21;  Length 1255;
  Best Local Similarity   73.2%;  Pred. No. 0;
  Matches  919;  Conservative    0;  Mismatches    0;  Indels  336;  Gaps    1;

Qy          1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60

Qy         61 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120

Qy        121 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180

Qy        181 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240

Qy        241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300

Qy        301 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360
```

```
Qy        361 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP 420

Qy        421 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 480

Qy        481 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC 540

Qy        541 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC 600

Qy        601 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTS------- 653
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIISAVVG 660

Qy        654 ------------------------------------------------------------ 653

Db        661 ILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETEL 720

Qy        654 ------------------------------------------------------------ 653

Db        721 RKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSP 780

Qy        654 ------------------------------------------------------------ 653

Db        781 YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVR 840

Qy        654 ------------------------------------------------------------ 653

Db        841 LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT 900

Qy        654 ------------------------------------------------------------ 653

Db        901 HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM 960

Qy        654 ----------------------------QNEDLGPASPLDSTFYRSLLEDDDMGDLVDA 684
                                         ||||||||||||||||||||||||||||||
Db        961 IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA 1020

Qy        685 EEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG 744
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 EEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG 1080

Qy        745 AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV 804
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV 1140

Qy        805 NQPDVRPQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ 864
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 NQPDVRPQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ 1200

Qy        865 GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 919
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1255


RESULT 7
AAB85458
ID   AAB85458 standard; Protein; 1255 AA.
XX
AC   AAB85458;
XX
DT   25-SEP-2001  (first entry)
XX
DE   Human HER-2/neu protein.
XX
KW   Antigen-presenting cell; immunogenic; immune response; HER-2/neu;
KW   oncogene; cancer; cytostatic; vaccine; p185; c-erbB2.
XX
OS   Homo sapiens.
XX
PN   WO200153463-A2.
XX
PD   26-JUL-2001.
XX
PF   19-JAN-2001; 2001WO-US01850.
XX
PR   21-JAN-2000; 2000US-0177545.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Cheever MA,  Hand-Zimmermann S;
XX
DR   WPI; 2001-476112/51.
DR   N-PSDB; AAH23392.
XX
PT   New antigen-presenting cells, useful as vaccines for eliciting or
PT   enhancing an immune response to HER-2/neu protein, particularly useful
PT   for treating or preventing cancer, e.g. breast cancer  -
XX
PS   Claim 2; Page 41-46; 49pp; English.
XX
CC   The invention provides an isolated antigen-presenting cell, which
CC   expresses at least an immunogenic portion of a polypeptide that produces
CC   an immune response to HER-2/neu protein. The antigen-presenting cells are
CC   useful as vaccines for eliciting or enhancing an immune response to
CC   HER-2/neu protein, particularly in treating or preventing malignancies in
CC   which the HER-2/neu oncogene is associated. Specifically, these are
CC   useful for treating or preventing cancer, e.g. breast cancer, ovarian,
CC   colon, lung or prostate cancers. The present sequence represents
CC   the human HER-2/neu protein (also known as p185 or c-erbB2).
XX
SQ   Sequence   1255 AA;

  Query Match             96.5%;  Score 4900;  DB 22;  Length 1255;
  Best Local Similarity   73.2%;  Pred. No. 0;
  Matches  919;  Conservative    0;  Mismatches    0;  Indels  336;  Gaps    1;

Qy          1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60

Qy         61 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120

Qy        121 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180

Qy        181 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240

Qy        241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300

Qy        301 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360

Qy        361 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP 420

Qy        421 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 480
```

```
Qy        481 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC 540

Qy        541 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC 600

Qy        601 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTS------- 653
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIISAVVG 660

Qy        654 ------------------------------------------------------------ 653

Db        661 ILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETEL 720

Qy        654 ------------------------------------------------------------ 653

Db        721 RKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSP 780

Qy        654 ------------------------------------------------------------ 653

Db        781 YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVR 840

Qy        654 ------------------------------------------------------------ 653

Db        841 LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT 900

Qy        654 ------------------------------------------------------------ 653

Db        901 HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM 960

Qy        654 ----------------------------QNEDLGPASPLDSTFYRSLLEDDDMGDLVDA 684
                                           ||||||||||||||||||||||||||||||
Db        961 IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA 1020

Qy        685 EEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG 744
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 EEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG 1080

Qy        745 AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV 804
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV 1140

Qy        805 NQPDVRPQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ 864
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 NQPDVRPQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ 1200

Qy        865 GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 919
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1255
```

RESULT 8
AAG88267
ID AAG88267 standard; Protein; 1255 AA.
XX
AC AAG88267;
XX
DT 11-SEP-2001 (first entry)
XX
DE HER2/neu amino acid sequence.
XX
KW Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;
KW immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;
KW tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.
XX
OS Homo sapiens.
XX
PN WO200141787-A1.
XX
PD 14-JUN-2001.
XX
PF 11-DEC-2000; 2000WO-US33591.
XX
PR 10-DEC-1999; 99US-0458299.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;
PI Keogh E;
XX
DR WPI; 2001-374995/39.
XX
PT An isolated prepared HER2/neu epitope useful in a vaccine for inducing
PT cellular immune responses for the prevention and treatment of cancer -
XX
PS Disclosure; Page 15; 199pp; English.
XX
CC The present invention describes isolated prepared HER2/neu epitopes (I).
CC Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is
CC culture in vitro and binds to a complex of an epitope (I), bound to a
CC human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)
CC and a second epitope and the peptide is less than 50 contiguous amino
CC acids that have 100% identity with a native peptide sequence of HER2/neu;
CC (3) a vaccine composition (III) comprising (II) and a pharmaceutical
CC excipient; (4) an isolated nucleic acid encoding a peptide comprising
CC (I); and (5) an isolated nucleic acid encoding (II). (I) has cytostatic
CC and immunostimulant activities, and can be used in vaccines. (I), (II)
CC and (III) are useful for inducing cellular immune responses for the
CC prevention and treatment of cancer. (I) and (II) are useful for
CC monitoring or evaluating an immune response to a tumour-associated
CC antigen when incubated with a T lymphocyte sample form a patient and
CC detecting the presence of bound T lymphocyte to (I) or (II). Epitope
CC based vaccines mean that immunosuppressive epitopes that may be present
CC in whole antigens may be avoided. Selected epitopes may be combined to
CC enhance immunogenicity. The possible pathological side effects caused by
CC infectious agents or whole protein antigen is eliminated. The vaccine
CC provides the ability to direct and focus an immune response to multiple
CC selected antigens from the same pathogen. Epitope-based anti-tumour
CC vaccines provides the opportunity to combine epitopes derived from
CC multiple tumour-associated molecules addressing the problem of tumour-
CC tumour variability and reducing the likelihood of tumour escape due to
CC antigen loss. AAG88266 to AAG89121 represent amino acid sequences used in
CC the exemplification of the present invention.
XX
SQ Sequence 1255 AA;

Query Match 96.5%; Score 4900; DB 22; Length 1255;
Best Local Similarity 73.2%; Pred. No. 0;
Matches 919; Conservative 0; Mismatches 0; Indels 336; Gaps 1;

```
Qy          1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60

Qy         61 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120

Qy        121 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180

Qy        181 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240

Qy        241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300

Qy        301 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360
```

```
Qy        361 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP 420

Qy        421 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 480

Qy        481 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC 540

Qy        541 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC 600

Qy        601 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTS------- 653
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIISAVVG 660

Qy        654 ------------------------------------------------------------ 653

Db        661 ILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETEL 720

Qy        654 ------------------------------------------------------------ 653

Db        721 RKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSP 780

Qy        654 ------------------------------------------------------------ 653

Db        781 YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVR 840

Qy        654 ------------------------------------------------------------ 653

Db        841 LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT 900

Qy        654 ------------------------------------------------------------ 653

Db        901 HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM 960

Qy        654 ----------------------------QNEDLGPASPLDSTFYRSLLEDDDMGDLVDA 684
                                         ||||||||||||||||||||||||||||||
Db        961 IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA 1020

Qy        685 EEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG 744
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 EEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG 1080

Qy        745 AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV 804
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV 1140

Qy        805 NQPDVRPQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ 864
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 NQPDVRPQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ 1200

Qy        865 GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 919
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1255
```

RESULT 9
AAE24067
ID AAE24067 standard; Protein; 1255 AA.
XX
AC AAE24067;
XX
DT 23-SEP-2002 (first entry)
XX
DE Human Her-2 protein.
XX
KW Human; Her-2; epidermal growth factor receptor 2; infection; cancer;
KW hyperproliferative disorder; prophylaxis; inflammation; antisense;
KW tumour; gene therapy; phosphorothioate backbone.
XX
OS Homo sapiens.
XX
PN WO200222636-A1.
XX
PD 21-MAR-2002.
XX
PF 12-SEP-2001; 2001WO-US28572.
XX
PR 15-SEP-2000; 2000US-0663834.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Cowsert LM;
XX
DR WPI; 2002-471192/50.
DR N-PSDB; AAD38904.
XX
PT Novel antisense oligonucleotide which modulates the expression of Human
PT Epidermal Growth Factor receptor, Her2, is useful for treating tumors
PT inflammation or to prevent infection in humans -
XX
PS Example 13; Page 95-107; 116pp; English.
XX
CC The invention relates to antisense compounds targetted to a nucleic
CC acid molecule encoding Her2 (human Epidermal Growth Factor receptor 2)
CC that specifically hybridises with and inhibits the expression of Her2.
CC Antisense compounds of the invention are used for treating diseases or
CC conditions associated with Her2 such as hyperproliferative disorders
CC e.g. lung, breast, gastric, oesophageal, colon, bladder, salivary,
CC neural or cardiac cancer. They are also useful prophylactically e.g.
CC to prevent or delay infection, inflammation and tumour formation. The
CC invention is also used in gene therapy. The present sequence is human
CC Her-2 protein.
XX
SQ Sequence 1255 AA;

Query Match 96.5%; Score 4900; DB 23; Length 1255;
Best Local Similarity 73.2%; Pred. No. 0;
Matches 919; Conservative 0; Mismatches 0; Indels 336; Gaps 1;

```
Qy          1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60

Qy         61 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120

Qy        121 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180

Qy        181 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240

Qy        241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300

Qy        301 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360

Qy        361 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP 420

Qy        421 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 480
```

```
Qy        481 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC 540

Qy        541 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC 600

Qy        601 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTS------- 653
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIISAVVG 660

Qy        654 ------------------------------------------------------------ 653

Db        661 ILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETEL 720

Qy        654 ------------------------------------------------------------ 653

Db        721 RKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSP 780

Qy        654 ------------------------------------------------------------ 653

Db        781 YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVR 840

Qy        654 ------------------------------------------------------------ 653

Db        841 LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT 900

Qy        654 ------------------------------------------------------------ 653

Db        901 HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM 960

Qy        654 ----------------------------QNEDLGPASPLDSTFYRSLLEDDDMGDLVDA 684
                                           ||||||||||||||||||||||||||||||
Db        961 IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA 1020

Qy        685 EEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG 744
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 EEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG 1080

Qy        745 AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV 804
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV 1140

Qy        805 NQPDVRPQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ 864
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 NQPDVRPQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ 1200

Qy        865 GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 919
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1255
```

RESULT 10
AAE20479
ID AAE20479 standard; Protein; 1255 AA.
XX
AC AAE20479;
XX
DT 01-JUL-2002 (first entry)
XX
DE Human Her-2/neu protein.
XX
KW Human; Her-2/Neu protein; immune response; gene therapy; breast cancer;
KW human leukocyte antigen; HLA; vaccine; malignancy; cytostatic.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 1021..1030
FT /note= "Naturally processed HLA-B44-restricted epitope"
XX

PN WO200214503-A2.
XX
PD 21-FEB-2002.
XX
PF 14-AUG-2001; 2001WO-US41733.
XX
PR 14-AUG-2000; 2000US-225152P.
PR 28-SEP-2000; 2000US-236428P.
PR 21-FEB-2001; 2001US-270520P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Hand-zimmermann S, Cheever MA, Foy TM, Lodes MJ, Kalos MD;
PI Mcneill PD, Vedvick TS;
XX
DR WPI; 2002-280758/32.
DR N-PSDB; AAD32743.
XX
PT Novel isolated Her-2/Neu polypeptide composition useful for therapy,
PT prevention and diagnosis of cancer, preferably breast cancer -
XX
PS Disclosure; Page 114-117; 129pp; English.
XX
CC The invention relates to an isolated Her-2/Neu polypeptide composition
CC effective for eliciting an immune response. The invention is useful for
CC eliciting an immune response in a patient, where the patient is human
CC leukocyte antigen (HLA)-B44 positive or is affected with breast cancer.
CC The composition is useful for the therapy and diagnosis of cancer,
CC preferably breast cancer, in pharmaceutical compositions, e.g., vaccine
CC and other compositions for the diagnosis, prevention and treatment of
CC human malignancies, for stimulating and/or expanding T cells specific for
CC Her-2/Neu polypeptide and for inhibiting the development of cancer in a
CC patient. The invention is useful for stimulating a T cell response in a
CC human patient, as probe or primer for nucleic acid hybridisation, to
CC selectively form duplex molecules with complementary stretches of the
CC entire Her-2/Neu gene or gene fragments of interest, to isolate a full
CC length gene from a suitable library, and to direct expression of a
CC polypeptide in appropriate host cells. The composition is useful in
CC prophylactic or therapeutic applications and for the treatment of cancer,
CC preferably for the immunotherapy of breast cancer and other Her-2/Neu-
CC associated malignancies. The invention is useful in gene therapy. The
CC present sequence is human Her-2/neu protein.
XX
SQ Sequence 1255 AA;

Query Match 96.5%; Score 4900; DB 23; Length 1255;
Best Local Similarity 73.2%; Pred. No. 0;
Matches 919; Conservative 0; Mismatches 0; Indels 336; Gaps 1;

```
Qy          1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60

Qy         61 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120

Qy        121 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180

Qy        181 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240

Qy        241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300

Qy        301 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360
```

```
Qy        361 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP 420

Qy        421 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 480

Qy        481 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC 540

Qy        541 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC 600

Qy        601 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTS------- 653
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIISAVVG 660

Qy        654 ------------------------------------------------------------ 653

Db        661 ILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETEL 720

Qy        654 ------------------------------------------------------------ 653

Db        721 RKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSP 780

Qy        654 ------------------------------------------------------------ 653

Db        781 YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVR 840

Qy        654 ------------------------------------------------------------ 653

Db        841 LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT 900

Qy        654 ------------------------------------------------------------ 653

Db        901 HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM 960

Qy        654 ----------------------------QNEDLGPASPLDSTFYRSLLEDDDMGDLVDA 684
                                           ||||||||||||||||||||||||||||||
Db        961 IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA 1020

Qy        685 EEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG 744
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 EEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG 1080

Qy        745 AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV 804
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV 1140

Qy        805 NQPDVRPQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ 864
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 NQPDVRPQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ 1200

Qy        865 GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 919
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1255
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```
RESULT 11
AAM51143
ID   AAM51143 standard; Protein; 1255 AA.
XX
AC   AAM51143;
XX
DT   17-JUN-2002  (first entry)
XX
DE   Human Her-2/neu oncogene-encoded p185 glycoprotein.
XX
KW   Her-2/neu; oncogene; cancer; tumour; vaccine; human; p185;
KW   tyrosine kinase; receptor; c-erbB2; gene therapy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Domain          1..653
FT                   /note= "extracellular domain"
FT   Domain          676..1255
FT                   /note= "intracellular domain"
FT   Domain          990..1255
FT                   /note= "phosphorylation domain"
XX
PN   WO200212341-A2.
XX
PD   14-FEB-2002.
XX
PF   03-AUG-2001; 2001WO-US24283.
XX
PR   03-AUG-2000; 2000US-0632507.
XX
PA   (CORI-) CORIXA CORP.
PA   (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI   Cheever MA,  Gheysen D;
XX
DR   WPI; 2002-241743/29.
DR   N-PSDB; ABA92250.
XX
PT   Her-2/neu fusion protein for treating or preventing cancer by eliciting
PT   or enhancing an immune response to the protein, has Her-2/neu
PT   extracellular domain fused to Her-2/neu intracellular or
PT   phosphorylation domain  -
XX
PS   Claim 68; Fig 7; 141pp; English.
XX
CC   The present sequence is that of human Her-2/neu (p185 glycoprotein
CC   or c-erbB2), an oncogenic self-protein and target for anti-cancer
CC   vaccines.  The Her-2/neu gene is amplified and p185 is overexpressed
CC   in a variety of cancers, including breast, ovarian, colon, lung and
CC   prostate cancer.  Her-2/neu is a member of the tyrosine kinase
CC   family of receptor-like glycoproteins.  It comprises an extracellular
CC   domain with homology to the epidermal growth factor receptor
CC   (EGFR), a highly hydrophobic transmembrane domain and a C-terminal
CC   intracellular domain that also shows homology to EGFR.  Its
CC   overexpression correlates with a poor prognosis in breast and
CC   ovarian cancers.  The invention provides Her-2/neu fusion
CC   proteins, nucleic acids encoding them, viral vectors, and vaccines
CC   comprising the fusion proteins or nucleic acid molecules.  In
CC   preferred fusion proteins, the extracellular domain of a Her-2/neu
CC   protein is fused to a Her-2/neu intracellular domain or
CC   phosphorylation domain (or its DeltaPD fragment).  An immune
CC   response to Her-2/neu protein is elicited or enhanced by
CC   administering the fusion protein in the form of a vaccine, or by
CC   transfecting cells of an animal ex vivo with a nucleic acid
CC   encoding the fusion protein, and delivering the transfected cells
CC   to the animal.  The fusion proteins, nucleic acids, and isolated
CC   specific T-cells are useful for inhibiting the development of a
CC   cancer, especially breast, ovarian, colon, lung or prostate cancer
CC   in a patient.  T cells that specifically react with a Her-2/neu
CC   fusion protein can be used to remove tumour cells from a sample in
CC   order to inhibit the development of cancer in a patient.
XX
SQ   Sequence   1255 AA;

  Query Match           96.5%;  Score 4900;  DB 23;  Length 1255;
  Best Local Similarity   73.2%;  Pred. No. 0;
  Matches  919;  Conservative    0;  Mismatches    0;  Indels  336;  Gaps    1;

Qy          1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60

Qy         61 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db        61 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120

Qy       121 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180

Qy       181 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240

Qy       241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300

Qy       301 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360

Qy       361 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP 420

Qy       421 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 480
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Db       421 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 480

Qy       481 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC 540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       481 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC 540

Qy       541 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC 600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       541 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC 600

Qy       601 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTS------- 653
             |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       601 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIISAVVG 660

Qy       654 ------------------------------------------------------------ 653

Db       661 ILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETEL 720

Qy       654 ------------------------------------------------------------ 653

Db       721 RKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSP 780

Qy       654 ------------------------------------------------------------ 653

Db       781 YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVR 840

Qy       654 ------------------------------------------------------------ 653

Db       841 LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT 900

Qy       654 ------------------------------------------------------------ 653

Db       901 HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM 960

Qy       654 ----------------------------QNEDLGPASPLDSTFYRSLLEDDDMGDLVDA 684
                                        ||||||||||||||||||||||||||||||||
Db       961 IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA 1020

Qy       685 EEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG 744
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 EEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG 1080

Qy       745 AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV 804
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1081 AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV 1140

Qy       805 NQPDVRPQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ 864
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1141 NQPDVRPQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ 1200

Qy       865 GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 919
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1201 GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1255
```

RESULT 12
AAU77114
ID AAU77114 standard; Protein; 1255 AA.
XX
AC AAU77114;
XX
DT 05-JUN-2002 (first entry)
XX
DE Human Her-2/neu polypeptide.
XX
KW Human; Her-2/neu; cytostatic; haematological malignancy; CML;
KW acute myelogenous leukaemia; AML; chronic myelogenous leukaemia; CLL;
KW chronic lymphocytic leukaemia; myeloma; non-Hodgkin's lymphoma; MDS;
KW Hodgkin's lymphoma; T cell therapy.
XX
OS Homo sapiens.
XX
PN WO200213847-A2.
XX
PD 21-FEB-2002.
XX
PF 13-AUG-2001; 2001WO-US25408.
XX
PR 14-AUG-2000; 2000US-0638280.
PR 28-SEP-2000; 2000US-0675904.
XX
PA (CORI-) CORIXA CORP.
XX
PI Gaiger A, Cheever MA, Hand-zimmermann S;
XX
DR WPI; 2002-280741/32.
DR N-PSDB; ABK10730.
XX
PT Inhibiting haematological malignancy development by administering
PT polypeptide comprising immunogenic portion of Her-2/neu, polynucleotide
PT encoding the polypeptide, or antigen presenting cells expressing the
PT polypeptide -
XX
PS Disclosure; Page 71-74; 74pp; English.
XX
CC The invention relates to a method for inhibiting development of
CC haematological malignancy in a patient by administering a polypeptide
CC comprising an immunogenic portion of Her-2/neu or a polynucleotide
CC encoding the polypeptide. Antigen presenting cells that express the
CC protein can also be administered. The sequences are used for inhibiting
CC development of haematological malignancy such as acute myelogenous
CC leukaemia (AML), chronic myelogenous leukaemia (CML), chronic lymphocytic
CC leukaemia (CLL), MDS, myelomas, Hodgkin's lymphoma and non-Hodgkin's
CC lymphoma. This sequence represents the human Her-2/neu polypeptide.
XX
SQ Sequence 1255 AA;

Query Match 96.5%; Score 4900; DB 23; Length 1255;
Best Local Similarity 73.2%; Pred. No. 0;
Matches 919; Conservative 0; Mismatches 0; Indels 336; Gaps 1;

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Qy         1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60

Qy        61 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120

Qy       121 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180
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Qy      181 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240

Qy      241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300

Qy      301 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360

Qy      361 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP 420

Qy      421 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 480

Qy      481 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC 540

Qy      541 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC 600

Qy      601 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTS------- 653
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIISAVVG 660

Qy      654 ------------------------------------------------------------ 653

Db      661 ILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETEL 720

Qy      654 ------------------------------------------------------------ 653

Db      721 RKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSP 780

Qy      654 ------------------------------------------------------------ 653

Db      781 YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVR 840

Qy      654 ------------------------------------------------------------ 653

Db      841 LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT 900

Qy      654 ------------------------------------------------------------ 653

Db      901 HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM 960

Qy      654 ----------------------------QNEDLGPASPLDSTFYRSLLEDDDMGDLVDA 684
                                         ||||||||||||||||||||||||||||||
Db      961 IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA 1020

Qy      685 EEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG 744
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Db     1021 EEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG 1080

Qy      745 AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV 804
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1081 AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV 1140

Qy      805 NQPDVRPQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ 864
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1141 NQPDVRPQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ 1200

Qy      865 GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 919
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1201 GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1255
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RESULT 13
AAY92620
ID   AAY92620 standard; Protein; 1255 AA.
XX
AC   AAY92620;
XX
DT   10-AUG-2000  (first entry)
XX
DE   Human heregulin 2 (Her2).
XX
KW   Heregulin 2; Her2; vaccination; cytotoxic T-lymphocyte immunity;
KW   self-protein; cancer; breast cancer; prostate cancer;
KW   cell-associated peptide antigen; foreign epitope.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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FT                   /note= "mature polypeptide"
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FT   Region          103..117
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FT                   /note= "suitable for foreign epitope insertion"
FT   Region          149..163
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FT                   /note= "suitable for foreign epitope insertion"
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FT   Region          210..224
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FT   Domain          484..623
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FT   Region          579..593
FT                   /label= insertion_region
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FT   Domain          624..654
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FT   Region          632..652
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FT                   /note= "suitable for foreign epitope insertion"
FT   Region          653..667
FT                   /label= insertion_region
FT                   /note= "suitable for foreign epitope insertion"
FT   Domain          655..1010
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FT   Region          695..709
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FT                   /note= "suitable for foreign epitope insertion"
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FT                   /note= "suitable for foreign epitope insertion"
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FT                   /label= C-terminal_domain
XX
PN   WO200020027-A2.
XX
PD   13-APR-2000.
XX
PF   05-OCT-1999;   99WO-DK00525.
XX
PR   05-OCT-1998;   98DK-0001261.
PR   20-OCT-1998;   98US-0105011.
XX
PA   (MEBI-) M & E BIOTECH AS.
XX
PI   Steinaa L,  Mouritsen S,  Nielsen KG,  Haaning J,  Leach D,  Dalum I;
PI   Gautam A,  Birk P,  Karlsson G;
XX
DR   WPI; 2000-349917/30.
DR   N-PSDB; AAA09455.
XX
PT   Inducing immune responses to weakly immunogenic, tumor associated
PT   peptide antigens for the treatment of breast and prostate cancer
XX
PS   Claim 62; Page 193-198; 220pp; English.
XX
CC   This is the human heregulin 2 (Her2) sequence. Immunogenic analogues of
CC   Her2 can be used in the claimed method as an autovaccine to induce a CTL
CC   response.  Subdominant CTL epitopes, antibody binding regions and
CC   cysteine residues involved in disulfide bonds are preserved in the
CC   immunogenized forms.  Regions suitable for the insertion of foreign T
CC   helper epitopes were identified (see features table).  The method
CC   is used for inducing immune responses against weakly immunogenic
CC   cell-associated peptide antigens (PA) such as those associated with
CC   cancers (self-proteins), e.g. human prostate specific membrane antigen
CC   (PSM), heregulin 2 (Her2) and/or fibroblast growth factor 8b (FGF8b).
CC   The method comprises effecting simultaneous presentation by antigen
CC   producing cells (APCs) of the animals immune system of: (1) at least 1
CC   CTL (cytotoxic T-lymphocyte) group derived from the PA and/or at least 1
CC   B-cell group derived from the cell-associated PA; and (2) at least 1
CC   first T helper cell group which is foreign to the animal.  Analogues of
CC   human PSM, human Her2 and human/murine FGF8b comprising a substantial
CC   part of all known and predicted CTL and B-cell epitopes of the respective
CC   PA and including at least one foreign T helper epitope are also claimed.
CC   The method is used to treat prostate, prostate/breast or breast cancer
CC   when the PA is human PSM, FGF8b and Her2, respectively.
XX
SQ   Sequence   1255 AA;

  Query Match             96.3%;  Score 4892;  DB 21;  Length 1255;
  Best Local Similarity   73.1%;  Pred. No. 0;
  Matches  918;  Conservative    0;  Mismatches    1;  Indels  336;  Gaps    1;

Qy          1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60

Qy         61 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120

Qy        121 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180

Qy        181 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240

Qy        241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300

Qy        301 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360

Qy        361 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP 420

Qy        421 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 480
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 480

Qy        481 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC 540
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC 540

Qy        541 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC 600
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC 600

Qy        601 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTS------- 653
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVSAVVG 660

Qy        654 ------------------------------------------------------------ 653

Db        661 ILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETEL 720

Qy        654 ------------------------------------------------------------ 653

Db        721 RKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSP 780

Qy        654 ------------------------------------------------------------ 653

Db        781 YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVR 840

Qy        654 ------------------------------------------------------------ 653

Db        841 LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT 900

Qy        654 ------------------------------------------------------------ 653

Db        901 HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM 960

Qy        654 ----------------------------QNEDLGPASPLDSTFYRSLLEDDDMGDLVDA 684
                                           |||||||||||||||||||||||||||||||
Db        961 IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA 1020

Qy        685 EEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG 744
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 EEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG 1080

Qy        745 AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV 804
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV 1140

Qy        805 NQPDVRPQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ 864
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db       1141 NQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ 1200

Qy        865 GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 919
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1255


RESULT 14
AAE12130
ID   AAE12130 standard; Protein; 1255 AA.
XX
AC   AAE12130;
XX
```

```
DT   18-DEC-2001  (first entry)
XX
DE   Human tyrosine kinase-type receptor, HER-2.
XX
KW   Therapeutic compound; major histocompatibility complex; vaccine;
KW   antigenic peptide; MHC; immunoregulatory; immune response; HER-2;
KW   adoptive immunotherapy; anti-cancer; breast cancer antigen; APC;
KW   antigen presenting cell; human; tyrosine kinase-type receptor.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          774..782
FT                   /note= "Antigenic epitope"
XX
PN   WO200168677-A2.
XX
PD   20-SEP-2001.
XX
PF   16-MAR-2001; 2001WO-US40328.
XX
PR   16-MAR-2000; 2000US-0527487.
XX
PA   (GENZ ) GENZYME CORP.
XX
PI   Nicolette CA;
XX
DR   WPI; 2001-616284/71.
DR   N-PSDB; AAD19731.
XX
PT   Novel synthetic therapeutic compound for inducing immune response and
PT   for use in adoptive immunotherapy, has enhanced binding to major
PT   histocompatibility molecules and enhanced immunoregulatory properties
PT   -
XX
PS   Claim 4; Page 63-67; 69pp; English.
XX
CC   The invention relates to synthetic therapeutic compounds (antigenic
CC   peptides) with enhanced binding to major histocompatibility complex
CC   (MHC) molecules and enhanced immunoregulatory properties relative
CC   to their natural counterparts. Compounds of the invention are useful
CC   for inducing an immune response in a subject and for use in adoptive
CC   immunotherapy. They are useful as components of anti-cancer vaccines
CC   and to expand immune effector cells that are specific for cancers
CC   characterised by expression of the breast cancer antigen, HER-2.
CC   Polynucleotides that encode peptides of the invention are useful as
CC   hybridisation probes and as primers for the detection of genes of gene
CC   transcripts that are expressed in antigen presenting cells (APCs), to
CC   confirm transduction of polynucleotides into host cells. The present
CC   sequence is human tyrosine kinase-type receptor, HER-2. Compounds
CC   of the invention are designed based on the HER-2 antigenic peptide
CC   (774-782).
XX
SQ   Sequence   1255 AA;

  Query Match             96.3%;  Score 4892;  DB 22;  Length 1255;
  Best Local Similarity   73.1%;  Pred. No. 0;
  Matches  918;  Conservative    0;  Mismatches    1;  Indels  336;  Gaps    1;

Qy          1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60

Qy         61 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120

Qy        121 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180

Qy        181 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        181 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240

Qy        241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300

Qy        301 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360

Qy        361 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP 420

Qy        421 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 480
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 480

Qy        481 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC 540
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC 540

Qy        541 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC 600
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC 600

Qy        601 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTS------- 653
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVSAVVG 660

Qy        654 ----------------------------------------------------------- 653

Db        661 ILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETEL 720

Qy        654 ----------------------------------------------------------- 653

Db        721 RKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSP 780

Qy        654 ----------------------------------------------------------- 653

Db        781 YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVR 840

Qy        654 ----------------------------------------------------------- 653

Db        841 LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT 900

Qy        654 ----------------------------------------------------------- 653

Db        901 HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM 960

Qy        654 ----------------------------QNEDLGPASPLDSTFYRSLLEDDDMGDLVDA 684
                                           |||||||||||||||||||||||||||||||
Db        961 IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA 1020

Qy        685 EEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG 744
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 EEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG 1080

Qy        745 AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV 804
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV 1140

Qy        805 NQPDVRPQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ 864
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       1141 NQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ 1200

Qy        865 GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 919
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1255

RESULT 15
AAB60167
```

```
ID   AAB60167 standard; Protein; 1255 AA.
XX
AC   AAB60167;
XX
DT   03-APR-2001  (first entry)
XX
DE   HER2 transgene plasmid construct encoded protein.
XX
KW   Human; HER2; ErbB2 receptor; p185neu; maytansinoid conjugate; cancer;
KW   antibody.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200100244-A2.
XX
PD   04-JAN-2001.
XX
PF   23-JUN-2000; 2000WO-US17229.
XX
PR   25-JUN-1999;  99US-0141316.
PR   16-MAR-2000; 2000US-0189844.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Erickson S,  Schwall R;
XX
DR   WPI; 2001-061962/07.
DR   N-PSDB; AAF24297.
XX
PT   Treating tumors, particularly breast cancers, which overexpress an ErbB
PT   receptor and does not respond to an anti-ErbB antibody, comprises
PT   conjugating the antibody to a maytansinoid -
XX
PS   Example 3; Fig 4; 92pp; English.
XX
CC   The present invention provides a method of treating cancer by
CC   administering a conjugate of anti-ErbB antibody with a maytansinoid. In
CC   particular, the antibody is directed against ErbB2 (also known as HER2
CC   and p185neu). The method is particularly useful in the treatment of
CC   breast, ovarian, stomach, endometrial, salivary gland, lung, kidney,
CC   colon, colorectal, thyroid, pancreatic, prostate and bladder cancers.
XX
SQ   Sequence   1255 AA;

  Query Match           96.3%;  Score 4892;  DB 22;  Length 1255;
  Best Local Similarity   73.1%;  Pred. No. 0;
  Matches  918;  Conservative    0;  Mismatches    1;  Indels  336;  Gaps    1;

Qy          1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60

Qy         61 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120

Qy        121 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180

Qy        181 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240

Qy        241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300

Qy        301 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360

Qy        361 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP 420

Qy        421 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 480

Qy        481 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC 540

Qy        541 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC 600

Qy        601 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTS------- 653
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVSAVVG 660

Qy        654 ------------------------------------------------------------ 653

Db        661 ILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETEL 720

Qy        654 ------------------------------------------------------------ 653

Db        721 RKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSP 780

Qy        654 ------------------------------------------------------------ 653

Db        781 YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVR 840

Qy        654 ------------------------------------------------------------ 653

Db        841 LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT 900

Qy        654 ------------------------------------------------------------ 653

Db        901 HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM 960

Qy        654 ----------------------------QNEDLGPASPLDSTFYRSLLEDDDMGDLVDA 684
                                           ||||||||||||||||||||||||||||||
Db        961 IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA 1020

Qy        685 EEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG 744
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 EEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG 1080

Qy        745 AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV 804
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV 1140

Qy        805 NQPDVRPQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ 864
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db       1141 NQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ 1200

Qy        865 GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 919
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1255


Search completed: December  5, 2003, 14:33:14
Job time : 59.6401 secs
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